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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:26:58 ; Search time 10.93 Seconds
(without alignments)
239.825 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171
Sequence: 1 MASQKRPQSHGSKYLTATAS.....SKIFKLGGRDSHGSPMARR 171

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 152396 seqs, 15329161 residues

Word size : 0

Total number of hits satisfying chosen parameters: 152396

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents,AA:*
1: /cgnl_7/prodata/1/1aa/5A_COMB.pep:*
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3: /cgnl_7/prodata/1/1aa/6_COMB.pep:*
4: /cgnl_7/prodata/1/1aa/PCRTUS_COMB.pep:*
5: /cgnl_7/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	171	100.0	171	2	US-08-781-122-2
2	170	99.4	170	2	US-08-327-357A-1
3	63	36.8	168	5	5194425-4
4	41	24.0	170	1	US-08-227-372-1
5	41	24.0	170	3	US-08-470-397-1
6	41	24.0	170	5	5194425-3
7	40	23.4	40	3	US-08-297-395-2
8	26	15.2	170	5	5468481-3
9	24	14.0	24	2	US-08-480-190-46
10	24	14.0	24	2	US-08-468-379-46
11	24	14.0	24	4	PCT-US93-07545-46
12	23	13.5	23	1	US-08-787-547-1
13	21	12.3	21	1	US-08-787-547-33
14	20	11.7	20	1	US-08-227-372-4
15	20	11.7	20	1	US-08-787-547-34
16	20	11.7	20	1	US-08-787-547-35
17	20	11.7	20	1	US-08-787-547-40
18	20	11.7	20	2	US-08-640-344-6
19	20	11.7	20	2	US-08-640-344-8
20	20	11.7	20	2	US-08-640-344-9
21	20	11.7	20	2	US-08-468-540B-1
22	20	11.7	20	2	US-08-468-540B-2
23	20	11.7	20	2	US-08-468-540B-4
24	20	11.7	20	2	US-08-468-540B-5
25	20	11.7	20	2	US-08-468-540B-10
26	20	11.7	20	2	US-08-468-540B-11
27	20	11.7	20	2	US-08-468-540B-13
28	20	11.7	20	2	US-08-606-639A-5

29	20	11.7	20	3	US-08-470-397-4	Sequence 4, Appl
30	20	11.7	20	3	US-08-297-395-14	Sequence 14, Appl
31	20	11.7	20	3	US-08-297-395-15	Sequence 15, Appl
32	20	11.7	20	3	US-08-297-395-16	Sequence 16, Appl
33	20	11.7	20	3	US-08-297-395-17	Sequence 17, Appl
34	20	11.7	20	3	US-08-297-395-18	Sequence 18, Appl
35	20	11.7	20	3	US-08-297-395-19	Sequence 19, Appl
36	20	11.7	20	3	US-08-297-395-20	Sequence 20, Appl
37	20	11.7	20	3	US-08-297-395-21	Sequence 21, Appl
38	20	11.7	20	3	US-08-297-395-22	Sequence 22, Appl
39	20	11.7	20	3	US-08-297-395-23	Sequence 23, Appl
40	20	11.7	20	3	US-08-297-395-25	Sequence 25, Appl
41	19	11.1	19	2	US-08-640-344-2	Sequence 2, Appl
42	19	11.1	19	2	US-08-468-540B-9	Sequence 9, Appl
43	19	11.1	19	2	US-08-468-540B-12	Sequence 12, Appl
44	19	11.1	19	3	US-08-297-395-1	Sequence 1, Appl
45	19	11.1	19	3	US-08-297-395-24	Sequence 24, Appl

ALIGNMENTS

```
RESULT 1
US-08-781-122-2
; Sequence 2, Application US/08781122
; Patent No. 5948764
;
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
; TITLE OF INVENTION: UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,122
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Markl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 690068.418C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-781-122-2

Query Match 100.0%; Score 171; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 4e-160;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MASQKRPQSHGSKYLTATASMDHARGFLPRHRDGIILDSIGRFGDGGARGGSKD 60
DB 1 MASQKRPQSHGSKYLTATASMDHARGFLPRHRDGIILDSIGRFGDGGARGGSKD 60
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QY 61 SHHPTAHYGSILPQKSHGRTODENPVHFFKNITVPRTPPSQKGRGLSLSRFSWGAE 120
DB 61 SHHPTAHYGSILPQKSHGRTODENPVHFFKNITVPRTPPSQKGRGLSLSRFSWGAE 120
QY 121 GORPGGYGGRASDYKSAHKGFYVDAQGLTSLKIFKLGDRSRSGSPMAR 171
DB 121 GORPGGYGGRASDYKSAHKGFYVDAQGLTSLKIFKLGDRSRSGSPMAR 171

RESULT 2

US-08-327-357A-1
Sequence 1, Application US/08327357A
Patent No. 5817629

GENERAL INFORMATION:
APPLICANT: WARREN, Kenneth G.
APPLICANT: CATZ, Ingrid
TITLE OF INVENTION: PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
TITLE OF INVENTION: PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
TITLE OF INVENTION: PEPTIDES TO MULTIPLE SCLEROSIS PATIENTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,357A
FILING DATE: 21-OCT-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,099
FILING DATE: 27-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 2,053,799-0
FILING DATE: 22-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Immen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 27052-115469
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: human myelin basic protein
US-08-327-357A-1

Query Match 99.4%; Score 170; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.8e-159;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRSQHGKSYLTASTMDHARGLFLPRHDTGLDLSIGRFGDGAPKRGSGKDS 61
DB 1 ASQKRSQHGKSYLTASTMDHARGLFLPRHDTGLDLSIGRFGDGAPKRGSGKDS 60
QY 62 HHPTAHYGSILPQKSHGRTODENPVHFFKNITVPRTPPSQKGRGLSLSRFSWGAE 121

DB 61 HHPTAHYGSILPQKSHGRTODENPVHFFKNITVPRTPPSQKGRGLSLSRFSWGAE 120
QY 122 GORPGGYGGRASDYKSAHKGFYVDAQGLTSLKIFKLGDRSRSGSPMAR 171
DB 121 GORPGGYGGRASDYKSAHKGFYVDAQGLTSLKIFKLGDRSRSGSPMAR 170

RESULT 3

5194425-4

Patent No. 5194425
APPLICANT: SHARMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
BRIAN R.

TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/367,751
FILING DATE: 21-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
SEQ ID NO: 4
LENGTH: 168
5194425-4

Query Match 36.8%; Score 63; DB 5; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.1e-54;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 GLSLRFSWGAGORPGGYGGRASDYKSAHKGFYVDAQGLTSLKIFKLGDRSRSGSPM 168
DB 106 GLSLRFSWGAGORPGGYGGRASDYKSAHKGFYVDAQGLTSLKIFKLGDRSRSGSPM 165
QY 169 ARR 171
DB 166 ARR 168

RESULT 4

US-08-227-372-1
Sequence 1, Application US/08227372
Patent No. 5763585

GENERAL INFORMATION:
APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..170
OTHER INFORMATION: /note="Myelin basic protein"
US-08-227-372-1

Query Match 24.0%; Score 41; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.1e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 QDENPVVHFFKNIVTPRPPSGKGRGLSRSFSGAEGQ 122
Db 81 QDENPVVHFFKNIVTPRPPSGKGRGLSRSFSGAEGQ 121

RESULT 5
US-08-470-397-1
Sequence 1, Application US/08470397
Patent No. 6007820
GENERAL INFORMATION:
APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: Purification and Characterization of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,397
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,372
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1

OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="Xaa - N-acetyl-alanine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product="OTHER"
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NAME/KEY: Modified-site
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OTHER INFORMATION: /product="OTHER"
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NAME/KEY: Modified-site
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NAME/KEY: Modified-site
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NAME/KEY: Modified-site
LOCATION: 66
OTHER INFORMATION: /product="OTHER"
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NAME/KEY: Modified-site
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NAME/KEY: Modified-site
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 141
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 144
OTHER INFORMATION: /product="OTHER"
OTHER INFORMATION: /note="Xaa - His or Val"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..170
OTHER INFORMATION: /note="Myelin basic protein"
US-08-470-397-1

Query Match 24.0%; Score 41; DB 3; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.1e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSWGAEQ 122
DB 81 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSWGAEQ 121

RESULT 6
5194425-3
; Patent No. 5194425
; APPLICANT: SHANMA, SOMESH D.; LERCH, L. BERNARD; CLARK,
; BRIAN R.
; TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
; AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/367,751
; FILING DATE: 21-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; SEQ ID NO:3:
; LENGTH: 170
5194425-3

Query Match 24.0%; Score 41; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.1e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSWGAEQ 122
DB 81 QDENPVHFEKNTVPTPTPPSGKRGSLSRFSWGAEQ 121

RESULT 7
US-08-297-395-2
; Sequence 2, Application US/08297395A
; Patent No. 6039947
; GENERAL INFORMATION:
; APPLICANT: Howard L. Weiner
; APPLICANT: David A. Hailer
; TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
; FILE REFERENCE: 1010/05723US3
; CURRENT APPLICATION NUMBER: US/08/297,395A
; CURRENT FILING DATE: 1994-08-11
; EARLIER APPLICATION NUMBER: 08/059,189
; EARLIER FILING DATE: 1993-05-06
; EARLIER APPLICATION NUMBER: 07/502,559
; EARLIER FILING DATE: 1990-03-30
; EARLIER APPLICATION NUMBER: PCT/US88/02139
; EARLIER FILING DATE: 1988-06-24
; EARLIER APPLICATION NUMBER: 07/065,734
; EARLIER FILING DATE: 1987-06-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-297-395-2

Query Match 23.4%; Score 40; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.9e-32;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 SLPOKSHGRTDQDENPVHFEKNTVPTPTPPSGKRGSL 111
DB 51 SLPOKSHGRTDQDENPVHFEKNTVPTPTPPSGKRGSL 111

DB 1 SLPOKSHGRTDQDENPVHFEKNTVPTPTPPSGKRGSL 40

RESULT 8
5468481-3
; Patent No. 5468481
; APPLICANT: SHANMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L.
; TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL
; IN AMELIORATING AUTOIMMUNITY
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,293
; FILING DATE: 14-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 690,840
; FILING DATE: 23-APR-1991
; APPLICATION NUMBER: 576,084
; FILING DATE: 30-AUG-1990
; APPLICATION NUMBER: 210,594
; FILING DATE: 23-JUN-1988
; APPLICATION NUMBER: 635,840
; FILING DATE: 28-DEC-1998
; APPLICATION NUMBER: 367,751
; FILING DATE: 21-JUN-1989
; SEQ ID NO:3:
; LENGTH: 170
5468481-3

Query Match 15.2%; Score 26; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 3.4e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 DAQGLSKIFKIGRDSRSGSPMAR 171
DB 145 DAQGLSKIFKIGRDSRSGSPMAR 170

RESULT 9
US-08-480-190-46
; Sequence 46, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Darlo A. A. Vignelli
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-46

Query Match 14.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 5,4e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRGDENPVVHFFKNIVTPRTPP 102
Db 1 GRGDENPVVHFFKNIVTPRTPP 24
|||||

RESULT 10
US-08-488-379-46
Sequence 46, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

US-08-488-379-46

Query Match 14.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 5,4e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRGDENPVVHFFKNIVTPRTPP 102
Db 1 GRGDENPVVHFFKNIVTPRTPP 24
|||||

RESULT 11
PCT-US93-07545-46
Sequence 46, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-46

Query Match 14.0%; Score 24; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5,4e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRGDENPVVHFFKNIVTPRTPP 102
Db 1 GRGDENPVVHFFKNIVTPRTPP 24
|||||

RESULT 12
US-08-787-547-1
Sequence 1, Application US/08787547
Patent No. 5783567

```

GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-1

Query Match      13.5%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 5e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GRTODENPVVHFKNVTPTPTTP 101
DB 1 GRTODENPVVHFKNVTPTPTTP 23

RESULT 13
US-08-787-547-33
Sequence 33, Application US/08787547
Patent No. 5783567
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Langer, Robert S.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
```

```

OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-787-547-33

Query Match      12.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SQRHSGKYLATSTMDHARG 28
DB 1 SQRHSGKYLATSTMDHARG 21
```

```

RESULT 14
US-08-227-372-4
Sequence 4, Application US/08227372
Patent No. 5763585
GENERAL INFORMATION:
APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF
TITLE OF INVENTION: MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,372
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14058-32-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-227-372-4

Query Match 11.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 GFGYGRASDYKSAHKFGK 144
|||||
DB 1 GFGYGRASDYKSAHKFGK 20

RESULT 15

US-08-787-547-34
; Sequence 34, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-34

Query Match 11.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 RDTGILDSIGRFFGGDRGAP 53
|||||
DB 1 RDTGILDSIGRFFGGDRGAP 20

Search completed: September 26, 2000, 19:36:55
Job time: 597 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:26:53 ; Search time 11.86 Seconds

(without alignments)
341.511 Million cell updates/sec

Title: US-09-218-277-12

Sequence: 1 MASQKRPSQRHSGSKYLATAS.....SKIFKLGRDSRSGSPMARR 171

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 188963 seqs, 23686106 residues

Word size : 0

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	171	1	R97627 Human myelin basic
2	171	100.0	171	1	R99580 Human myelin basic
3	170	99.4	170	1	R48592 Human myelin basic
4	170	99.4	170	1	R95406 Human myelin basic
5	113	66.1	197	1	W00399 Human myelin basic
6	113	66.1	203	1	W06107 Foetal myelin basi
7	113	66.1	203	1	W06108 Foetal myelin basi
8	113	66.1	373	1	W06103 MP4 chimera (MBP21
9	113	66.1	375	1	W06104 PM4 chimera (delta
10	113	66.1	385	1	W06102 MP3 chimera (MBP21
11	113	66.1	492	1	W06105 MMOGP4 chimera (MB
12	92	53.8	170	1	R30736 Human MBP. Pure ma
13	86	50.3	170	1	R35440 Human basic myelin
14	63	36.8	168	1	R04717 Empirically determ
15	46	26.9	46	1	W72360 Human myelin basic
16	46	26.9	167	1	R48595 Human myelin basic
17	45	26.3	127	1	R48596 Rat myelin basic p
18	45	26.3	168	1	R48594 Rabbit myelin basi
19	41	24.0	170	1	R02226 Myelin basic prote
20	41	24.0	170	1	R30735 Bovine MBP. Pure m
21	41	24.0	170	1	R45947 Myelin basic prote
22	41	24.0	170	1	W57236 Myelin basic prote
23	33	19.3	169	1	R48593 Cattle myelin basi
24	32	18.7	32	1	R85138 Human MBP residues
25	32	18.7	32	1	R95369 Residues 139-170 o
26	27	15.8	27	1	R95372 Residues 142-168 o
27	26	15.2	170	1	R86422 Myelin basic prote
28	25	14.6	25	1	R85135 Human MBP residues
29	25	14.6	25	1	R95371 Residues 142-166 o
30	25	14.6	25	1	R95367 Residues 111-135 o
31	25	14.6	25	1	R95342 MBP-2.5 (80-104).
32	25	14.6	25	1	R95346 MBP-4 (141-165). M
33	25	14.6	25	1	R95347 MBP-5 (101-125). M

34	25	14.6	25	1	W43948 Human myelin basic
35	25	14.6	25	1	W43952 Human myelin basic
36	25	14.6	25	1	W43953 Human myelin basic
37	24	14.0	24	1	R49336 Myelin basic prote
38	24	14.0	24	1	MBP-2.1 (82-105).
39	24	14.0	24	1	R74158 Antigenic peptide
40	24	14.0	24	1	W37554 Human myelin basic
41	24	14.0	24	1	W54719 Peptide from myel
42	23	13.5	23	1	R85137 Human MBP residues
43	23	13.5	23	1	MBP-2.2 (82-104).
44	23	13.5	23	1	MBP-2.6 (80-102).
45	23	13.5	23	1	MBP-2 (83-105). My

ALIGNMENTS

RESULT 1	
R97627	1
ID	R97627 standard; Protein; 171 AA.
AC	R97627;
DT	09-NOV-1996 (first entry)
DE	Human myelin basic protein.
KW	Myelin basic protein; MBP; multiple sclerosis; MS; treatment; prevention; analogue.
OS	Homo sapiens.
FX	Key
FT	Peptide
FN	Location/Qualifiers
FD	86..99
FE	/Label- Claimed peptide region.
PR	W0616085-A1.
PR	30-MAR-1996.
PR	16-NOV-1995; U14402.
PR	18-NOV-1994; US-342078.
PA	(NEUR-) NEUROCRINE BIOSCIENCES INC.
PI	(STRD) UNIV STANFORD MEDICAL CENT.
PI	Conlon PJ, Gaur A, Ling N, Steinman L;
DR	WPI; 96-268534/27.
DR	N-PSDB; T30269.
PT	Peptide analogue of human myelin basic protein - has lysine 91
PS	Replaced by another amino acid, useful to treat multiple sclerosis
CC	Claim 1: Figure 1: 30pp: English.
CC	A peptide analogue comprising amino acids 87-99 of human myelin
CC	basic protein (MBP), where lys91 is substituted for another amino
CC	acid can be used to treat and prevent multiple sclerosis. The
CC	peptide analogue is administered at a dosage range of 5-50 mg/kg.
SO	Sequence 171 AA;
Query Match	100.0%; Score 171; DB 1; Length 171;
Best Local Similarity	100.0%; Pred. No. 5.7e-161;
Matches 171; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 MASQKRPSQRHSGSKYLATASMDARHGFPRHRDTGLDSTGRFGGDRAPKRGSKD 60
DB	1 MASQKRPSQRHSGSKYLATASMDARHGFPRHRDTGLDSTGRFGGDRAPKRGSKD 60
OY	61 SHHPRTAHYGSLPQKSHGRQDENPVVHFPPKNTVPTPPSOGKGLSRSFSGAE 120
DB	61 SHHPRTAHYGSLPQKSHGRQDENPVVHFPPKNTVPTPPSOGKGLSRSFSGAE 120
OY	121 GORPEFGYGRASDYKSAHKGFGVDAQGLTSKIFKLGRDSRSGSPMARR 171
DB	121 GORPEFGYGRASDYKSAHKGFGVDAQGLTSKIFKLGRDSRSGSPMARR 171
RESULT 2	
R99580	
ID	R99580 standard; Protein; 171 AA.
AC	R99580;
DT	07-NOV-1996 (first entry)
DE	Human myelin basic protein (MBP).
KW	Myelin basic protein; MBP; multiple sclerosis; MS; competition; inhibition; major histocompatibility complex; MHC; thymocyte; T cell;

KW experimental allergic encephalomyelitis; EAE; analogue.
 OS Homo sapiens.
 PN WO9616086-A1.
 PD 30-MAY-1996.
 PF 16-NOV-1995; U14403.
 PR 18-NOV-1994; US-342408.
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
 PI Conlon PJ, Gaur A, Ling N, Steitman L;
 DR WPI; 96-268535/27.
 PT Peptide analogues of human myelin basic protein - useful for
 treatment of multiple sclerosis
 PS Disclosure: Figure 1, 61pp; English.
 CC Peptide analogues comprising at least seven amino acids from
 CC residues 86-99 of human myelin basic protein (MBP), can be used to
 CC treat multiple sclerosis by competing for the binding of native MBP
 CC peptide to MHC and by not causing proliferation of an MBP reactive T-
 CC cell line. The peptide analogues also inhibit the induction of
 CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.
 CC The peptide analogues have a reduced susceptibility to proteolysis
 CC in vivo.
 SQ Sequence 171 AA;

Query Match 100.0%; Score 171; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 5.7e-161;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKD 60
 1 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKD 60
 DB 1 MASQRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKD 60

QY 61 SHHPARTAHYGSGLPQKSHGRTODENPVVHFFKNIVTPRTPPPSQGKRGSLSRFSWGAE 120
 61 SHHPARTAHYGSGLPQKSHGRTODENPVVHFFKNIVTPRTPPPSQGKRGSLSRFSWGAE 120
 DB 61 SHHPARTAHYGSGLPQKSHGRTODENPVVHFFKNIVTPRTPPPSQGKRGSLSRFSWGAE 120

QY 121 GQRGFGYGRASDYKSAHKGFKGVDAOGTSLKIFKLGSDSGSPMARR 171
 121 GQRGFGYGRASDYKSAHKGFKGVDAOGTSLKIFKLGSDSGSPMARR 171
 DB 121 GQRGFGYGRASDYKSAHKGFKGVDAOGTSLKIFKLGSDSGSPMARR 171

RESULT 3
 R48592
 ID R48592 standard; protein: 170 AA.
 AC R48592;
 DE 31-JUL-1994 (first entry)
 KM Human myelin basic protein.
 KM Proteolipid protein: myelin basic protein; retrovirus;
 KM neurological disease; by-stander antigen; TGF-beta;
 KM transforming growth factor-beta; T-cell; T-lymphocyte;
 KM myelopathy; paraparesis; human immunodeficiency virus type 1.
 OS Homo sapiens.
 PN WO9404121-A.
 PD 03-MAR-1994.
 PF 17-AUG-1993; US-931217.
 PR 17-AUG-1993; US-931217.
 PA (AUTO-) AUTOIMMUNE INC.
 PI Hafler DA, Weiner HL;
 DR WPI; 94-082786/10.
 PT Treating retroviral associated neurological disease - by admin.
 PT of by-stander antigen, causing release of transforming growth
 PT factor beta from suppressor T cells
 PS Disclosure: Page 49; 64pp; English.
 CC Myelin basic proteins (sequences R48592-96) and cattle proteolipid
 CC protein (R48592) elicit the release of TGF-beta from suppressor T-
 CC cells and target the T-cells to neural tissue under cytotoxic
 CC attack, thereby reducing neurological disease, e.g. HTLV-1
 CC associated myelopathy, tropical spastic paraparesis and HIV
 CC infection.
 SQ Sequence 170 AA;

Query Match 99.4%; Score 170; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 5.5e-160;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKDS 61
 1 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKDS 60
 DB 1 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKDS 60

QY 62 HHHPARTAHYGSGLPQKSHGRTODENPVVHFFKNIVTPRTPPPSQGKRGSLSRFSWGAE 121
 62 HHHPARTAHYGSGLPQKSHGRTODENPVVHFFKNIVTPRTPPPSQGKRGSLSRFSWGAE 120
 DB 62 HHHPARTAHYGSGLPQKSHGRTODENPVVHFFKNIVTPRTPPPSQGKRGSLSRFSWGAE 120

QY 122 GQRGFGYGRASDYKSAHKGFKGVDAOGTSLKIFKLGSDSGSPMARR 171
 122 GQRGFGYGRASDYKSAHKGFKGVDAOGTSLKIFKLGSDSGSPMARR 170
 DB 122 GQRGFGYGRASDYKSAHKGFKGVDAOGTSLKIFKLGSDSGSPMARR 170

RESULT 4
 R95406
 ID R95406 standard; protein: 170 AA.
 AC R95406;
 DE 16-DEC-1996 (first entry)
 KM Myelin oligodendrocyte protein.
 KM Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
 KM CD4+, T-cell; autoimmune disease; demyelination; central nervous system;
 KM CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
 KM relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
 KM diabetes; Graves disease; myasthenia gravis; Good pasture's syndrome;
 KM psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
 KM myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
 OS Homo sapiens.
 PN WO9612737-A2.
 PD 02-MAY-1996.
 PF 25-OCT-1995; U13682.
 PR 25-OCT-1994; US-328224.
 PR 15-MAR-1995; US-404228.
 PR 25-OCT-1995; ZA-009033.
 PA (IMMU-) IMMULOGIC PHARM CORP.
 PI Devaux B, Franzen H, Hsu D, Pallard X;
 PI Rothbard J, Samson M, Shi J, Smlek D;
 DR WPI; 96-230552/23.
 PT Myelin basic derived peptide(s) and analogs - used in the treatment
 PT of Multiple Sclerosis, psoriasis, Graves Disease, etc.
 PS Example 9, Fig 1, 91pp; English.
 CC This sequence represents the human myelin oligodendrocyte protein (MOG).
 CC Immunisation with MOG (or the peptide fragments shown in R95375-R95385)
 CC can be used to induce experimental allergic encephalomyelitis (EAE) in
 CC susceptible strains of mice. EAE is a CD4+ T-cell mediated autoimmune
 CC disease which results in demyelination of the central nervous system,
 CC resulting in paralysis and other neurological abnormalities. EAE is a
 CC commonly used animal model for human multiple sclerosis (MS). These
 CC sequences can be used in compositions for treating MS in a mammal. The
 CC composition acts to down regulate the autoimmune response, and may be
 CC administered in an amount sufficient to prevent the onset of symptoms of
 CC MS. The compositions may also be used to treat advanced stage MS,
 CC especially relapsing-remitting MS, chronic progressive MS or benign MS.
 CC These peptides may also be used in the treatment of other diseases
 CC involving myelin autoantigens, including diabetes, Graves disease,
 CC myasthenia gravis, Good Pasture's syndrome, psoriasis, thyroiditis, and
 CC rheumatoid arthritis. Peptides derived from other myelin autoantigens,
 CC such as myelin basic protein (MBP, see R95334-R95374) proteolipid
 CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as
 CC alternatives to the MOG peptides in these compositions.
 SQ Sequence 170 AA;

Query Match 99.4%; Score 170; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 5.5e-160;
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKDS 61
 1 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKDS 60
 DB 1 ASQKRRPSQRHSGSKYLATASTMDHARHGFPRHRDTGILDSIGRFGGDBGAPRSGSKDS 60

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OY 62 HHPARTAHYGSIPKSHGRTODENPVHFFKNIVTPRTPPSGKRGRLSLSRFSWAG 121
    |||||||
DB 61 HHPARTAHYGSIPKSHGRTODENPVHFFKNIVTPRTPPSGKRGRLSLSRFSWAG 120
OY 122 QRPGRPGYGRASDYKSAHKFGKGVDAOGTSLKIRFKLGRDRSGSPMAR 171
    |||||||
DB 121 QRPGRPGYGRASDYKSAHKFGKGVDAOGTSLKIRFKLGRDRSGSPMAR 170

RESULT 5
W00399
ID W00399 standard; Protein; 197 AA.
AC W00399:
DT 01-FEB-1997 (first entry)
DE Human myelin basic protein (foetal isoform).
KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
KM multiple sclerosis; autoimmune disease; diagnosis; therapy;
OS T-lymphocyte; T-cell; energy; apoptosis.
FH Homo sapiens.
FH Key Location/Qualifiers
FT region 60..85
FT /label= X2
FT /note= "exon 2-encoded region"
FT misc_difference 81
FT /note= "Cys-81 may be replaced by any standard
FT amino acid, esp. an uncharged amino acid
FT of mol.wt. below about 150, partic.
FT Ser, in constructs of the invention"
PN W09634622-A1.
PD 07-NOV-1996.
PE 22-APR-1996: U05611.
PR 02-MAY-1995: US-431648.
PR 02-MAY-1995: US-431644.
PR 07-JUN-1995: US-482114.
PR (ALEX-) ALEXION PHARM INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
PI Nye SH, Peltrey CM, Squinto SP, Wilkins JA;
DR WPI: 96-505898/50.
DR N-PSDB: T41889.
PT New human myelin basic protein and proteolipid protein variant(s) -
PT used in the assessment, diagnosis and treatment of multiple
PT sclerosis
PS Claim 1; Page 79-80; 156pp; English.
CC The native human 21.5 kDa foetal isoform (W00399) of myelin basic
CC protein, MBP+X2Cys81, includes an exon 2-encoded region (X2) that
CC may contain an epitope involved in the pathogenesis of multiple
CC sclerosis (MS); the X2 region is not found in the MBP of healthy
CC adults. Recombinant MBP+X2, or variants modified to improve
CC bacterial expression (see also W06107), can be produced in a
CC large scale in bacterial hosts. They are useful for assaying
CC T-cells for responsiveness to MBP epitopes and can be used as
CC therapeutic agents that act by inducing T-cell responses.
CC including energy and apoptosis, as a means of treating MS.
SQ Sequence 197 AA;

```

```

AC W06107;
DT 01-FEB-1997 (first entry)
DE Foetal myelin basic protein MBP+X2Cys81/bact.
KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
KM multiple sclerosis; autoimmune disease; diagnosis; therapy;
OS Synthetic.
FH Key Location/Qualifiers
FT region 60..85
FT /label= X2
FT /note= "exon 2-encoded region"
PN W09634622-A1.
PD 07-NOV-1996.
PE 22-APR-1996: U05611.
PR 02-MAY-1995: US-431648.
PR 02-MAY-1995: US-431644.
PR 07-JUN-1995: US-482114.
PR (ALEX-) ALEXION PHARM INC.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
PI Nye SH, Peltrey CM, Squinto SP, Wilkins JA;
DR WPI: 96-505898/50.
DR N-PSDB: T41896.
PT New human myelin basic protein and proteolipid protein variant(s) -
PT used in the assessment, diagnosis and treatment of multiple
PT sclerosis
PS Disclosure; Page 81-82; 156pp; English.
CC A 21.5 kDa foetal isoform (W06107) of myelin basic protein.
CC MBP+X2Cys81/bact., is the product of a DNA construct (T41896)
CC based on the human foetal MBP+X2Cys81 isoform (W00399) but
CC utilizing bacterially-preferred codons in place of the native human
CC codons (see also T41889). This increases prodn. of the MBP in E.
CC coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also
CC W00399 and W06108) are useful in the clinical assessment, diagnosis
CC and treatment of MS.
SQ Sequence 203 AA;

Query Match
Best Local Similarity 100.0%; Pred. No. 8, 1e-104; Length 203;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 KDSHHPARTAHYGSIPKSHGRTODENPVHFFKNIVTPRTPPSGKRGRLSLSRFSW 118
    |||||||
DB 85 KDSHHPARTAHYGSIPKSHGRTODENPVHFFKNIVTPRTPPSGKRGRLSLSRFSW 144
OY 119 AEGORPGYGRASDYKSAHKFGKGVDAOGTSLKIRFKLGRDRSGSPMAR 171
    |||||||
DB 145 AEGORPGYGRASDYKSAHKFGKGVDAOGTSLKIRFKLGRDRSGSPMAR 197

RESULT 7
W06108
ID W06108 standard; Protein; 203 AA.
AC W06108;
DT 01-FEB-1997 (first entry)
DE Foetal myelin basic protein MBP+X2Ser81/bact.
KW Myelin basic protein; MBP; MBP+X2Ser81; proteolipid protein; PLP;
KM multiple sclerosis; autoimmune disease; diagnosis; therapy;
OS Synthetic.
FH Key Location/Qualifiers
FT region 60..85
FT /label= X2
FT /note= "exon 2-encoded region, with Cys81Ser
FT mutation"
FT /label= X2
FT /note= "Hexa-histidine tag
FT /note= "the hexa-histidine tag facilitates
FT purification of the recombinant protein
FT from host cells"
PN W09634622-A1.
PD 07-NOV-1996.

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PF 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PI (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP,
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR MPI: 96-505898/50.
 DR N-PSDB: T41897.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Disclosure: Page 82-83; 156pp; English.
 CC A 21.5 kda foetal isoform (W06108) of myelin basic protein,
 CC MBP+X2Ser81/bact., is the product of a DNA construct (T41897)
 CC based on the human foetal MBP+X2Cys81 isoform (W00399) but
 CC utilizing codons that are highly expressed in bacterial genes in
 CC place of the native codons (see also T41889) and incorporating a
 CC sequence coding for a hexa-histidine tail. This allows large-
 CC scale prodn. and purification of the MBP in bacterial hosts.
 CC Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) are
 CC useful in the clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 203 AA:

Query Match 66.1%; Score 113; DB 1; Length 203;
 Best Local Similarity 100.0%; Pred. No. 8; le-104;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KDSHPPARNAHYSLPSKSGRTQDENPVVHFKNITVPTPPPSOGKRGSLRSFSG 118
 DB 85 KDSHPPARNAHYSLPSKSGRTQDENPVVHFKNITVPTPPPSOGKRGSLRSFSG 144

QY 119 AEGORPFGYGGASDYKSAHKGFGVADGTLSTFKLGGRSRSQPMARR 171
 DB 145 AEGORPFGYGGASDYKSAHKGFGVADGTLSTFKLGGRSRSQPMARR 197

RESULT 8
 W06103
 ID W06103 standard; Protein: 373 AA.
 AC W06103;
 DT 01-FEB-1997 (first entry)
 DE MP4 chimera (MBP21.5-delta PLP4 fusion).
 KW Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
 KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KW therapy; T-lymphocyte; T-cell; energy; apoptosis; MP3 chimera.
 OS Synthetic.
 FH Key
 FT protein
 FT /note= "Location/Qualifiers
 FT /note= "Preferred protein of the invention"
 FT domain
 FT 1..197
 FT /label= MBP21.5
 FT peptide
 FT 198..200
 FT /label= Spacer
 FT domain
 FT 201..373
 FT /label= Delta_PLP4
 FT peptide
 FT 201..205
 FT /note= "synthetic N-terminal peptide not found in
 FT the native protein"
 FT region
 FT 208..219
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 210..230
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 241..261
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 242..255
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT /note= "PLP epitope associated with MS"

FT region
 FT 244..257
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 248..269
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 256..269
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 257..269
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 268..281
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 270..303
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 292..304
 FT /label= Epitope
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 FT 292..307
 FT /label= Epitope
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 FT region
 FT 295..306
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 314..326
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 326..337
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 326..339
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 351..365
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 213..234
 FT /label= Epitope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 256..269
 FT /label= Epitope
 FT /note= "encephalitogenic epitope in mouse model"
 FT region
 FT 292..304
 FT /label= Epitope
 FT /note= "encephalitogenic epitope in mouse model"
 FT peptide
 FT 369..373
 FT /label= Histidine_tag
 FT /note= "hexa-histidine tag facilitates recombinant
 FT protein purification"

W0634622-A1.
 PD 07-NOV-1996.
 PF 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP,
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR MPI: 96-505898/50.
 DR N-PSDB: T41893.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 34: Page 110-112; 156pp; English.
 CC MP4 chimera (W06103) is a fusion protein composed of human myelin
 CC basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and
 CC delta PLP4 (W06101), a proteolipid protein (PLP) mutein that lacks
 CC all 4 hydrophobic domains of native human PLP (W06106) but
 CC includes PLP epitopes associated with multiple sclerosis (MS). It

CC can be expressed in E. coli transformants using a DNA construct
 CC (T41893) contg. the MBP21.5-delta PLP4 gene fusion. MP4 chimera
 CC and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)
 CC are useful for the clinical assessment, diagnosis and treatment
 of MS.
 SQ Sequence 373 AA;

Query Match 66.1%; Score 113; DB 1; Length 373;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 KDSHHPARTAHYGLSPKSGRGTODENPVVHFFKNITVPTPTPPSGKRGSLSRFSWG 118
 DB 85 KDSHHPARTAHYGLSPKSGRGTODENPVVHFFKNITVPTPTPPSGKRGSLSRFSWG 144

OY 119 AEGORPFGYGRASDYKSAHKGFYDAOGTSLKIRKLGGRDSRSGSPMAR 171
 DB 145 AEGORPFGYGRASDYKSAHKGFYDAOGTSLKIRKLGGRDSRSGSPMAR 197

RESULT 9
 W06104
 ID W06104 standard: Protein; 375 AA.
 AC W06104:
 DT 01-FEB-1997 (first entry)
 DE PM4 chimera (delta PLP4-MBP21.5 fusion).
 KM Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;
 KM MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KM therapy: T-lymphocyte; T-cell; PM4 chimera.
 OS Synthetic.
 FH key
 FT Location/Qualifiers
 FT 6..374
 FT /note= "preferred PM4 chimera protein"
 FT 1..169
 FT /label= Delta-PLP4
 FT 1..5
 FT /note= "synthetic N-terminal peptide not found in
 FT the native protein"
 FT 9..20
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 11..31
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 42..62
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 43..60
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 45..58
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 49..70
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 57..70
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 58..71
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 59..82
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 71..104
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 93..105
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 93..108
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"

FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 96..107
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 115..127
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 127..138
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 127..140
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 152..166
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 14..35
 FT /label= Eptope
 FT /note= "encephalitogenic epitope in mouse model"
 FT 57..70
 FT /label= Eptope
 FT /note= "encephalitogenic epitope in mouse model"
 FT 93..105
 FT /label= Eptope
 FT /note= "encephalitogenic epitope in mouse model"
 FT 170..173
 FT /label= Spacer
 FT 174..368
 FT /label= MBP21.5
 FT 369..375
 FT /label= Histidine-tag
 FT /note= "hexa-histidine tag facilitates recombinant
 FT protein purification"
 W09634622-A1.
 PN 07-NOV-1996
 PD 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelitrey CM, Squinto SP, Wilkins JA;
 DR N-PDSB; T41894.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 35; Page 113-114; 156pp; English.
 CC PM4 chimera (W06104) is a fusion protein composed of delta PLP4
 CC (W06101) and MBP21.5 (W00399). Delta PLP4 is a proteolipid protein
 CC (PLP) mutant that lacks all 4 hydrophobic domains of native human
 CC PLP (W06106) but includes PLP epitopes associated with multiple
 CC sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic
 CC protein (MBP) associated with MS. PM4 is in reverse orientation to
 CC MP4 chimera (W06103). It can be expressed in bacterial host cells
 CC using a DNA construct (T41894). PLP polypeptides (see also W00400,
 CC W06101-03 and W06105) can be used in the clinical assessment,
 CC diagnosis and treatment of MS.
 SQ Sequence 375 AA;

Query Match 66.1%; Score 113; DB 1; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.3e-103;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 KDSHHPARTAHYGLSPKSGRGTODENPVVHFFKNITVPTPTPPSGKRGSLSRFSWG 118
 DB 257 KDSHHPARTAHYGLSPKSGRGTODENPVVHFFKNITVPTPTPPSGKRGSLSRFSWG 316
 OY 119 AEGORPFGYGRASDYKSAHKGFYDAOGTSLKIRKLGGRDSRSGSPMAR 171

Dd	317	AEGQRPGEYGGGRASDYKSAHKGFKGVDAOGILSKIFKLGGRDSRSGSMARR	369
<hr/>			
RESULT	10		
ID	W06102		
AC	W06102	standard; Protein: 385 AA.	
DT	01-FEB-1997	(first entry)	
DE	MP3 chimera (MBP21.5-delta PLP3 fusion).		
KM	Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;		
KW	MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;		
KV	therapy; T-lymphocyte; T-cell; atrophy; apoptosis; MP3 chimera.		
OS	Synthetic.		
FH	key	Location/Qualifiers	
FT	domain	1..197	/label= MBP21.5
FT	peptide	198..200	/label= Spacer
FT	domain	201..385	/label= Delta_PLP3
PN	W0634622-A1.		
PD	07-NOV-1996.		
PR	22-APR-1996:	U05611.	
PR	02-MAY-1995:	US-431648.	
PR	02-MAY-1995:	US-431644.	
PA	07-JUN-1995:	US-482114.	
PA	(ALEX-) ALEXION PHARM INC.		
PI	(US\$) US DEPT HEALTH & HUMAN SERVICES.		
PI	Lenaardo MJ, Mattis L, McFarland HF, Mueller EE, Mueller JP,		
PI	Nye SH, Palfrey CM, Squinto SP, Wilkins JA.		
MPI:	96-505896/50.		
DR	N-PDB: T41892.		
PT	New human myelin basic protein and proteolipid protein variant(s) -		
PT	used in the assessment, diagnosis and treatment of multiple		
PT	sclerosis		
PS	Claim 33; Page 108-110; 156pp; English.		
CC	MP3 chimera (W06102) is a fusion protein composed of human myelin		
CC	basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and		
CC	delta PLP3 (W00400), a proteolipid protein (PLP) muclein that lacks		
CC	hydrophobic domains 1, 3 and 4 of native human PLP (W06106) but		
CC	includes PLP epitopes associated with multiple sclerosis (MS). It		
CC	can be expressed in E. coli transformants using a DNA construct		
CC	(T41892) contg. the MBP21.5-delta PLP3 gene fusion. MP3 chimera		
CC	and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)		
CC	are useful for the clinical assessment, diagnosis and treatment		
CC	of MS.		
CC	Sequence 385 AA:		
SEQ			
<hr/>			
Query Match	66.1%; Score 113; DB 1; Length 385;		
Best Local Similarity	100.0%; Pred. No. 1.4e-103;		
Matches 113; conservative	0; Mismatches 0; Indels 0; Gaps 0;		
Oy	59 KDSHHPARTAHYGSGLPKSHGRTODENPVHFHKIVTPRTPEPPSGKRGSLSEFSWG	118	
Dd	85 KSHPHDPARTAHYAGSLPKSHGRTODENPVHFHKIVTPRTPEPPSGKRGSLSEFSWG	144	
Oy	119 AEGORPGFEYGGGRASDYKSAHKGFKGVDAOGILSKIFKLGGRDSRSGSMARR	171	
Dd	145 AEGORPGFEYGGGRASDYKSAHKGFKGVDAOGILSKIFKLGGRDSRSGSMARR	197	
<hr/>			
RESULT	11		
ID	W06105		
AC	W06105	standard; Protein: 492 AA.	
DT	01-FEB-1997	(first entry)	
DE	MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion).		
KM	Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;		
KW	MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;		
KV	therapy; T-lymphocyte; T-cell; MMOP4 chimera;		
KM	myelin oligodendrocyte glycoprotein; MOG.		
OS	Synthetic.		

FT	Key	Location/Qualifiers
FT	protein	1..487
FT		/note="preferred protein of the invention"
FT	domain	1..197
FT		/label="MAP21.5
FT	domain	198..319
FT		/label="MOG
FT	domain	/note="MOG extracellular domain"
FT		320..486
FT		/label="Delta_PLP4
FT	region	327..338
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	329..349
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	350..380
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	361..278
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	363..376
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	367..378
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	375..388
FT		/label="Epitope
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FT	region	376..388
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FT		/note="PLP epitope associated with MS"
FT	region	387..400
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	389..402
FT		/label="Epitope
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FT	region	411..423
FT		/label="Epitope
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FT		/label="Epitope
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FT	region	414..425
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	433..445
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FT	region	445..458
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	445..458
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	470..484
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	411..423
FT		/label="Epitope
FT		/note="PLP epitope associated with MS"
FT	region	487..492
FT		/label="Histidine tag
FT		/note="hexa-histidine tag facilitates recombinant

Protein purification

FT W09634622-A1.
 PN 07-NOV-1996.
 PD 22-APR-1996. U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matlis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI: 96-505898/50.
 DR N-PSDB: T41895.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 36; Page 115-117, 156pp; English.
 CC MMOGP4 chimera (W06105) is a fusion protein composed of human myelin
 CC basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the
 CC extracellular domain of human myelin oligodendrocyte glycoprotein
 CC (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutein.
 CC MBP21.5, PLP and MOG are all recognised by autoreactive T cells from
 CC multiple sclerosis (MS) patients. The chimera was produced using
 CC a DNA construct (T41895) obt. by inserting a sequence encoding the
 CC MOG moiety into MP4 chimera DNA (see also T41893). MMOGP4 chimera
 CC can be expressed in bacterial cell hosts. PLP and MBP polypeptides
 CC (see also W00400, W06101-04, W06107-08) are useful in the clinical
 CC assessment, diagnosis and treatment of MS.
 SQ Sequence 492 AA;

Query Match 66.1%; Score 113; DB 1; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.7e-103;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KDSHHPARTAHYGSLLPKRSKGTODENPVHFEKNIIVPRTPPPSGKGRGLSLRFSWG 118
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 DB 85 KDSHHPARTAHYGSLLPKRSKGTODENPVHFEKNIIVPRTPPPSGKGRGLSLRFSWG 144
 |||||||
 QY 119 AEGORPGFGYGRASDYKSAHKGFGVDAGTSLKIFKLGDRSGSPMAR 171
 |||||||
 DB 145 AEGORPGFGYGRASDYKSAHKGFGVDAGTSLKIFKLGDRSGSPMAR 197
 |||||||

RESULT 12
 ID R30736 standard; Protein; 170 AA.
 AC R30736;
 DT 21-MAY-1993 (first entry)
 DE Human MBP.
 KW Acetylcholine receptor; MHC; myelin basic protein; MBP.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT modified_site 1
 FT /note- "N-Ac-Ala"
 FT modified_site 107
 FT /note- "Me-Arg"
 FT peptide 1..14
 FT /note- "claim 30; page 68"
 PN W09218150-A.
 PD 29-OCT-1992.
 PR 23-APR-1992; U03391.
 PR 23-APR-1991; US-690840.
 PA (ANER-) ANERGEN INC.
 PI Clark BR, Lerch BL, Sharma SD;
 DR WPI: 93-036056/04.
 PT Pure major MHC-peptide complex - useful in treating deleterious
 PT immune response such as autoimmunity.
 PS Claim 30; Page 68 + Fig 7; 93pp; English.
 CC A method is claimed for the prep. of a pure major MHC-peptide
 CC complex. The MHC component is a class II glycoprotein of the MHC
 CC and the peptide comprises amino acids 1-14 of MBP.
 SQ Sequence 170 AA;

Query Match 53.8%; Score 92; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 3.3e-83;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 RTODENPVHFEKNIIVPRTPPPSGKGRGLSLRFSWGAEQORPGYGRASDYKSAH 139
 |||||||
 DB 79 RTODENPVHFEKNIIVPRTPPPSGKGRGLSLRFSWGAEQORPGYGRASDYKSAH 138
 |||||||
 QY 140 KGFKGVDAAGTSLKIFKLGDRSGSPMAR 171
 |||||||
 DB 139 KGFKGVDAAGTSLKIFKLGDRSGSPMAR 170
 |||||||

RESULT 13
 ID R35440 standard; Protein; 170 AA.
 AC R35440;
 DT 13-AUG-1993 (first entry)
 DE Human basic myelin protein.
 KW BMP; MS; multiple sclerosis; homologue; myelin basic protein; MBP.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 61..106
 FT /note- "neutralising fragment"
 FT peptide 1..15
 FT /note- "neutralising fragment"
 FT peptide 4..18
 FT /note- "neutralising fragment"
 FT peptide 9..23
 FT /note- "neutralising fragment"
 FT peptide 15..35
 FT /note- "neutralising fragment"
 FT peptide 20..37
 FT /note- "neutralising fragment"
 FT peptide 31..46
 FT /note- "neutralising fragment"
 FT modified_site 1
 FT /note- "acylated"
 PN W09308212-A.
 PD 29-APR-1993.
 PR 15-OCT-1992; CA0448.
 PR 22-OCT-1991; CA-053799.
 PA (CATZ/) CATZ I.
 PA (MAR/) WARREN K G.
 PI Catz I, Warren KG;
 DR WPI: 93-152422/18.
 PT Homologous peptide analogues of human basic myelin protein - used
 PT for treating multiple sclerosis
 PS Disclosure; Fig 4; 26pp; English.
 CC The sequence is that of human basic myelin protein (BMP). Fragments
 CC of this sequence are claimed (see features) which are able to
 CC neutralise anti-BMP antibodies and are thus useful in treatment of
 CC multiple sclerosis. The fragments may be prep. synthetically and
 CC avoids the dangers associated with the use of the natural protein,
 CC e.g. transmission of neuroviruses. Also the peptides are too small
 CC to be immunogenic.
 SQ Sequence 170 AA;

Query Match 50.3%; Score 86; DB 1; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.7e-77;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 PVHFEKNIIVPRTPPPSGKGRGLSLRFSWGAEQORPGYGRASDYKSAHKGFGV 145
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 DB 85 PVHFEKNIIVPRTPPPSGKGRGLSLRFSWGAEQORPGYGRASDYKSAHKGFGV 144
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 QY 146 DAOGTSLKIFKLGDRSGSPMAR 171
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 DB 145 DAOGTSLKIFKLGDRSGSPMAR 170
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RESULT 14
 ID R04717 standard; protein; 168 AA.
 AC R04717;
 DT 23-AUG-1990 (first entry)
 DE Empirically determined sequence of myelin basic protein (MBP)
 KM Myelin basic protein; multiple sclerosis; autoantigen; autoimmune disease;
 KW epitope; myelin sheath.
 FH key
 FT misc_difference 1
 FT /label=OTHER
 FT /note="N-Ac-Ala"
 FT misc_difference 168
 FT /label=OTHER
 FT /note="Arg-COOH"
 FT
 FT MO8912459-A.
 PN 28-DEC-1989.
 PF 23-JUN-1989; U02784.
 PR 21-JUN-1989; US-367751, US-210594.
 PA (Bios-) Biospan Corp.
 PI Sharma SD, Lerch LB, Clark BR;
 DR WPI; 90-022384/03.
 PT New complexes of histo-compatible glyco:protein -
 PT with antigenic peptide(s) and label or toxin, used to target
 PT antigen specific T helper cells
 PT Fig 7; ; 74pp; English.
 CC The patent claims complexes of formulae (I), (II) and (III) which are as
 CC follows: (I) X - MCH - peptide; (II) MHC - X; (III) MHC -
 CC peptide. Where X - toxin or labelling gp.; MHC - effective portion of the
 CC major histocompatibility glycoprotein; and the peptide includes an
 CC epitope associated with one of the major autoimmune diseases, including
 CC multiple sclerosis (MS). MBP is the principle autoantigen in MS and is a
 CC candidate peptide for insertion in the complexes which can be used to
 CC treat and monitor MS. Pertinent sections of MBP are determined
 CC empirically, using a strain of mice which develops experimental
 CC allergic encephalitis when immunised with bovine MBP. The sequence
 CC given in p94717 is with the substitution of the residues above the
 CC sequence in Fig 7. The sequence without substitutions is given in p92226.
 SQ Sequence 168 AA;

Query Match 36.8%; Score 63; DB 1; Length 168;
 Best Local Similarity 100.0%; Pred. No. 1.2e-54;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 GLSLSRFSWGAEQGRPGFGYGRASDYKSAHKGFGVDAQGLSKIFKLGDRSRSGSPM 168
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 DB 106 GLSLSRFSWGAEQGRPGFGYGRASDYKSAHKGFGVDAQGLSKIFKLGDRSRSGSPM 165
 QY 169 ARR 171
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 DB 166 ARR 168

RESULT 15
 ID W72360
 ID W72360 standard; peptide; 46 AA.
 AC W72360;
 DT 16-DEC-1998 (first entry)
 DE Human myelin basic protein fragment.
 KM Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS.
 OS Homo sapiens.
 PN W09845327-AL.
 PD 15-OCT-1998.
 PF 03-APR-1998; CA0290.
 PR 04-APR-1997; CA-201841.
 PA (UYAL-) UNIV ALBERTA.
 PI Catz I, Warren KG;
 DR WPI; 98-568356/48.
 PT Peptide and its derivatives for treatment of multiple sclerosis - 1s
 PT capable of neutralising or modulating production of anti-myelin
 PT basic protein

PS Disclosure; Page 15; 75pp; English.
 CC The present sequence represents a myelin basic protein (MBP) protein
 CC fragment used to produce MBP peptides. MBP peptides are capable of
 CC neutralising or modulating the production of anti-myelin basic protein.
 CC The present invention also describes a method for treating multiple
 CC sclerosis (MS). The method comprises administering to the patient an
 CC MBP peptide of the formula: R1-Val-His-Phe-Phe-Lys-Arg-Ile-R2 where R1,
 CC R2 = H, OH, or an amino acid residue and a polypeptide residue,
 CC provided that R1 and R2 are not both H or OH at the same time.
 SQ Sequence 46 AA;

Query Match 26.9%; Score 46; DB 1; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.2e-38;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 HHPARTAHYGSLLPQKSHGRTODENPVVHFFKNIIVPTPTPPSQGKG 107
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 DB 1 HHPARTAHYGSLLPQKSHGRTODENPVVHFFKNIIVPTPTPPSQGKG 46

Search completed: September 26, 2000, 19:36:37
 Job time: 584 sec

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Date: Sep 26, 2000 8:02 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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gb_pr3:HUM215MBP	+	899.00	1063.58	622	L41657 Homo sapiens synthetic m
gb_pr2:HUMMBPC	+	899.00	1058.54	1261	M30515 Human 21.5 KD myelin ba
gb_pr2:HUMMBP7K	+	847.50	998.74	1172	M30047 Human 17.3K myelin bas
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gb_ro:RNO132895	+	611.50	730.19	612	AJ132895 Rattus norvegicus m
gb_ro:RATMBP	+	611.50	720.71	387	AJ132895 Rattus norvegicus m
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gb_ro:RNO132896	+	588.50	701.94	2256	X17103 Chicken mRNA for myelin
gb_ov:RNO132896	+	588.50	701.94	465	AJ132896 Rattus norvegicus m
gb_ro:MUSMBP72M	+	581.50	693.38	1990	M5060 Mouse myelin basic prot
gb_ro:MUSGOLLIA	+	540.00	633.17	2490	L07507 Mouse Golli-mbp mRNA, c
gb_ov:AB000736	+	505.50	601.43	738	AB000736 Xenopus laevis mRNA, c
gb_pr2:HUMRNMBPE	+	330.50	333.90	1054	L18865 Human Golli-mbp gene, c
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gb_htg1:AP001773	+	330.50	335.87	166560	AP001773 Homo sapiens chrom
gb_htg1:AP001649	-	330.50	336.57	198597	AP001649 Homo sapiens chrom
gb_htg1:AP001853	+	330.50	336.41	203070	AP001853 Homo sapiens chrom
gb_ro:RNMBPX	+	319.50	333.04	195	X72392 R.norvegicus mbp mRNA, c
gb_ro:MUSMBP1	+	294.00	338.78	361	M1291 Mouse myelin basic prote
gb_ro:MUSGOLLIB	+	294.00	349.09	1407	L07508 Mouse Golli-mbp mRNA, c
gb_ro:MHMBPFG	+	294.00	340.54	7.2e-11	X67319 M.musculus mRNA for tra
gb_ro:MUSMBP1	+	284.00	330.99	1.9e-11	L00398 Mouse 14kd, 17kd, 18.5kd
gb_ov:HMBPA	+	283.50	338.02	1183	X17664 H.francisci mRNA for my
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DEFINITION Human Golli-mbp gene, complete cds.
ACCESSION L18866
VERSION L18866.1 GI:435061
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1781)
AUTHORS Pribyl,T.M., Campagnoni,C.W., Kampf,K., Kashima,T., Handley,V.W.,
McMahon,J. and Campagnoni,A.T.
TITLE The human myelin basic protein gene is included within a
179-kilobase transcription unit: expression in the immune and
central nervous systems
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (22), 10695-10699 (1993)
MEDLINE 94068468
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34 rGAspThrGlyLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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751 GGTGGCCCAAGCGGGCTCTGGCAAGGACTCACACCACCGCGCAAGAAC 800
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67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
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117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
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seq_name: gb_pr2:HUMMBPA

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DEFINITION Human myelin basic protein (MBP) mRNA, complete cds.
ACCESSION M13577
VERSION M13577.1 GI:187408
KEYWORDS myelin basic protein.
SOURCE Human brain, mRNA to cDNA, clones pMBP-1 and pMBP-2.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2139)
AUTHORS Kamholz,J., de Ferrá,F., Puckett,C. and Lazzarini,R.
TITLE Identification of three forms of human myelin basic protein by cDNA cloning
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)
MEDLINE 86259714
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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
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387 GGGGCGGAAGCCAGACAGCAGGATTTGGCTACGGAGGCGAGCGTCGC 436
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complete cds.
ACCESSION L41657
VERSION L41657.1 GI:1162921
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
Kamholz,J., de Ferra,F., Puckett,C. and Lazzarini,R.
Identification of three forms of human myelin basic protein by cDNA
cloning
Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (13), 4962-4966 (1986)
MEDLINE 86259714
REFERENCE
2 (bases 1 to 622)
Nye,S.H., Pelfrey,C.M., Burkwit,J.J., Voskuhl,R.R., Lenardo,M.J.
and Mueller,J.P.
Purification of immunologically active recombinant 21.5 kDa isoform
of human myelin basic protein
Mol. Immunol. 32 (14-15), 1131-1141 (1995)
JOURNAL Mol. Immunol. 32 (14-15), 1131-1141 (1995)
MEDLINE 96128281
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34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
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51 GlyAlaProLysArgGlySerGly..... 58
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154 GGTGCGCGAAACGTCGCTGTGGCAAGTGCCTGGCTGAAACCGGGCGC 203
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58 ..... 58
204 TAGCCCGCTGCCGCTCTCATGCCGTAGCCAGCGGGCCTGTGCAACATGT 253
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59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
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254 ACAAGACTCCACACCCCGGCTCGTACCGGCACACTATGGCTCCTCGCCG 303
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304 CAGAAATCCCGCGCGGTACCCAGGATGAAACCCGGTGGTGCACTTCTT 353
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354 CAAAACATTTGACCCCGCTAGCCCGCGCTCTCAGGCAAAAGGCC 403
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108 rGglyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
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404 GTGGCTGTCTCCTGAGCCGTTTCAGCTGGGCGCGGAAGCGCAGCGTCG 453
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125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
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454 GGCTTCGGCTACGGCGCGCGTGGCTCCGACTATAAATCTGTCAAAAGG 503
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141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
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504 CTTCAAGCGGTGGATGCCAGGCAACCTGTCCAAAATTTTCAAACTGG 553
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seq_name: gb_pr2:HUMMBPC

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seq_documentation_block:
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DEFINITION Human 21.5 kD myelin basic protein (RK41) mRNA, complete cds.
ACCESSION M30515
VERSION M30515.1 GI:187412
KEYWORDS alternative splicing; myelin basic protein.
SOURCE human spinal cord, cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1261)
Roth,H.J., Kronquist,K.E., Kerlero de Rosbo,N., Crandall,B.F. and
Campagnoni,A.I.
Evidence for the expression of four myelin basic protein variants
in the developing human spinal cord through cDNA cloning
J. Neurosci. Res. 17 (4), 321-328 (1987)
MEDLINE 87311781
FEATURES Location/Qualifiers
source 1..1261

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alignment_scores:

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Ratio: 5.257 Gaps: 1
Percent Similarity: 86.802 Percent Identity: 86.802

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8 ATGGCGCTCACAGAGAGACCTCCACAGAGCAGCATCCAAAGTACCTGGC 57
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHis 34
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58 CACAGCAAGTACCATGACCATCCAGCATGCTCTCTCCCAAGCACA 107
|||||
34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
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108 GAGACACGGGCATCTTGACTCCATCGGGCGCTCTTTGGCGGTGACAG 157
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51 GlyAlaProLysArgGlySerGly..... 58
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158 GGTGCGCCCAAGCGGGCTCTGCAAGGTACCTGGCTAAAGCGGCGCG 207
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58 ..... 58
208 GAGCCCTCTGCCCTCTCATGCCCCGACGACCTGGCTGTGCAACATGT 257
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59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
258 ACAAGGACTCACACCACCGCGCAAGACTGCTCCTATGCTCCCTGCC 307
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75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
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308 CAGAAGTCAACGCGCGGACCCCAAGATGAACACCCGCTAGTCCACTCTT 357
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358 CAAGAATTTGTACGCTCTGCACACACCCCGTGCAGGGAAGGGGA 407
|||||
108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
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408 GAGGACTGTCCCTGAGCAGATTTAGTGGGGCGCGCAAGGCCAGACCA 457
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125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
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458 GGATTTGGCTACGGAGGACAGCGTCCGACTATAAATCGGCTCACAGGG 507
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141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
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158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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seq_documentation_block:

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LOCUS HUMBP17K 1172 bp mRNA PRI 07-JAN-1995
DEFINITION Human 17.3K myelin basic protein (MBP) mRNA, complete cds.
ACCESSION M30047
VERSION M30047.1 GI:187400
KEYWORDS myelin basic protein.
SOURCE Human fetal spinal cord, cDNA to mRNA, clone KK36.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1172)
AUTHORS Roth,H.J., Kronquist,K., Pretorius,P.J., Crandall,B.F. and
Campagnoni,A.T.
TITLE Isolation and characterization of a cDNA coding for a novel human
17.3K myelin basic protein (MBP) variant
JOURNAL J. Neurosci. Res. 16 (1), 227-238 (1986)
MEDLINE 86308101
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/db_xref="GI:307162"
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BASE COUNT 273 a 353 c 306 g 240 t
ORIGIN

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alignment_scores:

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Quality: 847.50 Length: 171
Ratio: 5.297 Gaps: 1
Percent Similarity: 93.567 Percent Identity: 93.567

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alignment_block:

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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHis 34
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83 CACAGCAAGTACCATGAGCATGCCAGCATGCTCTCTCCCAAGCACA 132
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34 rGAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
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133 GAGACACGGGCATCTTGACTCCATCGGGCGCTCTTTGGCGGTGACAG 182
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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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183 GTTGGCGCCCAAGCGGGCTCTGGCAAGGACTCACACCACCGCGCAAGAC 232
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67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84

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233 TGCTCACTACGGCTCCCTGCCCAAGAAGTACACGGCGGAGCCCAAGATG 282
84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
283 AAAACCCCGTAGTCCACTCTCTTCAAGAACAATTGTGACGCCCTCGCACACCA 332
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
333 CCCCCCTCGCAGGGAAG..... 350
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyTyrGlyGlyArgAlaSerA 134
351 .GGGGCGGAAGCCAGACAGACCAGGATTGGCTACGGAGCGACAGGCTCG 399
134 spTyTyrSerAlaHisGlyGlyPheLysGlyValAspAlaGlnGlyThr 150
400 ACTATAAATCGGCTCACAGGGGATTCAGGGAGAGTCGATGCCAGGGCAG 449
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
450 CTTTCCAAAATTTTAACTGGGAGGAAGAGATAGTCGCTCTGGATCACC 499
167 oMetAlaArgArg 171
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seq_name: qb ro:RNO132897

seq_documentation_block:	510 bp	mRNA	ROD	11-FEB-1999
LOCUS	RNO132897	Rattus norvegicus mRNA for myelin basic protein, 18.5 kDa isoform.		
DEFINITION	Rattus norvegicus mRNA for myelin basic protein, 18.5 kDa isoform.			
ACCESSION	AJ132897			
VERSION	AJ132897.1	GI:4454314		
KEYWORDS	isoform; mbp gene; myelin; myelin basic protein.			
SOURCE	Norway rat			
ORGANISM	Rattus norvegicus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
AUTHORS	1 (bases 1 to 510)			
TITLE	Lobell, A.M.			
JOURNAL	Direct Submission			
	Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute, Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm, SWEDEN			
REFERENCE	2 (bases 1 to 510)			
AUTHORS	Lobell, A.M. and Wigzell, H.			
JOURNAL	Unpublished			
FEATURES	Location/Qualifiers			
source	1..510			

[illegible]

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Percent Similarity: 97.674      Percent Identity: 93.605
alignment_block:
US-09-218-277-12 x RNO132897  ..

Align seg 1/1 to: RNO132897 from: 1 to: 510

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17  aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
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51  CACAGCAAGTACCATTGGACCATCGCGGATGGCTCTCTCCCAAGGCACA 100

34  rgaspThrGlyIleLeuAspSerIleGlyArgPhePheGlyAspArg 50
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101  GAGACACGGGCATCTTGACTTCATCGCGCGCTCTTTACGCGGTGACAGG 150

51  GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
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151  GGTGGCCCCAAGCGGGGCTCTGSCAAGGACTCACAC.....ACAAGAAC 194

67  rAlaHisTyrlGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
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195  TACCCACTACGGCTCCCTGCCCCAGAGTCTGGAG...AGGACCCAGATG 241

84  luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
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242  AAAACCCAGTAGTCCTCTTCAAGAACATTGTGACACCTCGTACACCC 291

101  ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
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292  CCTCATCTCCCAAGGAAGGGGAGAGGCGCTGCCTCAGCAGATTAGCTG 341

117  pGlyAlaGluGlyClnArgProGlyPheGlyTyrlGlyArgAlaSerA 134
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342  GGGGGCCGAGGGGCGAAGAACCGAGATTGGCTACGGAGCAGAGCTTCGG 391

134  spTyrlsSerAlaHisLysGlyPheLysGlyVal...AspAlaGlnGly 149
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392  ACTATAATCGGCTCACAAGGGATTCAGGGGGGCGCTACAGCGCCACGGC 441

150  ThrLeuSerLysIlePheLysLeuGlyArgAspSerArgSerGlyse 166
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442  ACGCTTTCCAAAATCTTTAAGCTGGGAGGAAGACAGACGCCGCTCTGATC 491

166  rProMetAlaArg 171
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492  TCCCATAGCAAGACGC 507

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seq_name: qb_pr2:HUMMBPB

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DEFINITION	Human 20.2 kD myelin basic protein (RK187)		mrna,	complete cds.	
ACCESSION	M30516				
VERSION	M30516.1	GI:187410			
KEYWORDS	alternative splicing;	myelin basic protein.			
SOURCE	Human spinal cord,	cDNA to mRNA.			
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Mammalia;			
	Eutheria; Primates; Chordarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 1231)				
AUTHORS	Roth,H.J., Kronquist,K.E., Kerlero de Rosbo,N., Crandall,B.F. Campagnoni,A.T.				
TITLE	Evidence for the expression of four myelin basic protein varia				
JOURNAL	In the developing human spinal cord through cDNA cloning				
MEDLINE	J. Neurosci. Res. 17 (4), 321-328 (1987)				
FEATURES	87311781	Location/Qualifiers			
source	1..1231	/organism="Homo sapiens"			
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BASE COUNT 281 a 374 c 323 g 253 t
ORIGIN

alignment_scores:
Quality: 824.50 Length: 197
Ratio: 5.153 Gaps: 2
Percent Similarity: 81.218 Percent Identity: 81.218

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61 CACAGCAAGTACCATGACCATGCCAGCATGGCTTCTCCCAAGGCACA 110
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34 rGAspThrGlyLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
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111 GAGACAGGGCATCTTGACTCCATCCATCGGGCGCTTCTTTGGCGGTGACAGG 160
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51 GlyAlaProLysArgGlySerGly..... 58
161 GGTGCGCCCAAGCGGGCTCTGGCAAGGTACCTGGCTAAAGCGGGCGG 210
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58 ..... 58
211 GAGCCCTCTGCCCTCTCATGCCCGCAGCCAGCCTGGGCTGTGCAACATGT 260
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59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
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261 ACAAGGACTCACACACCGCGCAAGAACTGTCTACCTACGGCTCCCTGCC 310
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75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
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361 CAAGAACAATTGTGACGCTCGCACACACCCCGCTCGCAGGGAAG.... 406
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141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
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158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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seq_name: gb_ro:RNO132898

seq_documentation_block:
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DEFINITION Rattus norvegicus mRNA for myelin basic protein, 21.5 kDa isoform.
ACCESSION AJ132898
VERSION AJ132898.1 GI:4454316
KEYWORDS isoform; mbp gene; myelin; myelin basic protein.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
REFERENCE 1 (bases 1 to 588)
AUTHORS Weissert,R., Lobell,A.M., de Graaf,K.L., Eltayeb,S.Y.,
Andersson,R., Olesen,T. and Wigzell,H.
TITLE Protective DNA vaccination against organ-specific autoimmunity is
highly specific and discriminates between single amino acid
substitutions in the peptide autoantigen
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97, 1668-1694 (2000)
REFERENCE 2 (bases 1 to 588)
AUTHORS Lobell,A.M.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
SWEDEN

FEATURES
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BASE COUNT 148 a 184 c 160 g 96 t
ORIGIN

alignment_scores:
Quality: 813.00 Length: 198
Ratio: 4.839 Gaps: 4
Percent Similarity: 84.848 Percent Identity: 81.313

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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51 CACAGCAAGTACCATGGACCATGCCCGCATGGCTTCTCCCAAGGCACA 100
|||||
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
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101 GAGACAGGGCATCTTGACTCCATCGGGCGCTTCTTTAGCGGTGACAGG 150
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51 GlyAlaProLysArgGlySerGly..... 58
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 58 58
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 59 ..LysAspSerHisProAlaAlaThrAlaHisTyrGlySerLeuPro 74
 251 ACAAGGACTCACAC.....ACAAGAACTACCCACTACGGCTCCCTGGCC 294
 75 GlnLysSerHisGlyAlaThrGlnAspGluAsnProValHisPhePh 91
 295 CAGAACTCCAG...AGGACCCAAAGTGAACCCAGTAGTCCACTTC 341
 91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
 342 CAAGAACTTGTGACACCTCGTACACCCCTCCATCCCAAGGAAGGGGA 391
 108 rgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
 392 GAGGCTGTCCCTACACAGATTAGCTGGGGCCGAGGGCGCAGAGCCA 441
 125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
 442 GGAATTGGCTACGAGGCGAGCTCCGACTATAAATCGCTCACAAAGG 491
 141 yPheLysGlyVal...AspAlaGlnGlyThrLeuSerLysIlePheLys 157
 492 ATTCAAGGGGCTACGAGCCCGAGGCGACGCTTCCAAAATCTTTAAGC 541
 157 euGlyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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seq_name: gb_ro:AF074337

seq_documentation_block: 450 bp mRNA ROD 14-JUL-1998
 LOCUS AF074337 Cavia porcellus myelin basic protein (MBP) mRNA, partial cds.
 DEFINITION AF074337
 ACCESSION AF074337
 VERSION AF074337.1 GI:3309628
 KEYWORDS domestic guinea pig.
 SOURCE Cavia porcellus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 1 (bases 1 to 450)
 Kim,G., Tanuma,N. and Matsumoto,Y.
 DNA vaccination using Guinea pig myelin basic protein coding region
 in experimental autoimmune encephalomyelitis
 Unpublished
 2 (bases 1 to 450)
 Kim,G., Tanuma,N. and Matsumoto,Y.
 Direct Submission
 Submitted (24-JUN-1998) Neuropathology, Tokyo Metropolitan
 Institute for Neuroscience, Musashidai 2-6, Fuchu, Tokyo 183-8526,
 Japan
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 BASE COUNT 119 a 134 c 122 g 75 t
 ORIGIN

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 Quality: 724.50 Length: 154
 Ratio: 4.895 Gaps: 4
 Percent Similarity: 96.104 Percent Identity: 91.558

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 US-09-218-277-12 x AF074337 ..

Align seg 1/1 to: AF074337 from: 1 to: 450

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 24 sAlaArgHisGlyPheLeuProArgHisArgAspThrGlyIleLeuAsp 41
 51 TCCAGGCATGGCTTCTCCCAAGGCACAGACACAGGCATCCTTGACT 100
 41 erIleGlyArgPhePheGlyGlyAspArgGlyAlaProLysArgGlySer 57
 101 CCATCGGGCGCTTCTTGGCAGTGACAGGCTGCGCCCAAGCGGGCTCC 150
 58 GlyLysAspSerHisGlyProAlaArgThrAlaHisTyrGlySerLeuPr 74
 151 GGCAGGACTCACATCAGCAGCAAGACGACCCACTATGGCTCCCTGCC 200
 74 oGlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPheP 91
 201 CCAGAACTGCAG...CGGTCCCAAGATGAAACCCCTGTAGTCCACTTCT 247
 91 heLysAsnIleValThrProArgThrProProSerGlnGlyLysGly 107
 248 TCAAGAACAATTGTGACACCCCGCACACCTCTCCGTCTCAAGGAAGGA 297
 108 ArgGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPr 124
 298 AGAGGATTGTCCCTCAGCAGATTAGCTGGGAGCGCGAGGGCAGAAACC 347
 124 oGlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
 348 AGGATTGGCTATGGAGCGAGAGCT...GACTACAAATCC.....AAGG 388
 141 lyPheLysGlyVal...AspAlaGlnGlyThrLeuSerLysIlePheLys 156
 389 GATTCAAGGGGCGCCATGATGATGCCAGGCGACGCTTCCAAAATCTTAAA 438
 157 LeuGlyGlyArg 160
 439 CTGGGAGGAAGA 450
 seq_name: gb_ro:MUSMBP78M

seq_documentation_block: 1939 bp mRNA ROD 15-AUG-1995
 LOCUS MUSMBP78M Mouse myelin basic protein mRNA, 3' end, clone NK-M78.
 DEFINITION M15062
 ACCESSION M15062
 VERSION M15062.1 GI:199050
 KEYWORDS alternative splicing; myelin basic protein.
 SOURCE Mus musculus (strain C57BL/6J, sub-species domesticus) (clone: NK-M78.) 18-day-old brain cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1939)
 Newmann,S., Kitamura,K. and Campagnoni,A.T.

TITLE Identification of a cDNA coding for a fifth form of myelin basic protein in mouse

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84 (3), 886-890 (1987)

MEDLINE 87118269

COMMENT Draft entry and computer-readable sequence for [1] kindly provided by A.T. Campagnoni, 30-MAR-1987.

As many as eight myelin basic proteins can be encoded by the same gene by alternative splicing. The sequence below is missing exons 2 and 5 of the gene and encodes a 17.22 kDa myelin basic protein. The variations in the 3' untranslated regions between the two clones may be reverse transcriptase errors [1].

FEATURES Location/Qualifiers

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CDS

1023

/note="t in M78; c in M72"

/replace="c"

1700

/note="t in M78; c in M72"

/replace="c"

variation

variation

BASE COUNT 447 a 545 c 517 g 428 t 2 others

ORIGIN 35 bp upstream of AvarII site.

alignment_scores:

Quality: 716.50 Length: 161

Ratio: 4.908 Gaps: 4

Percent Similarity: 90.683 Percent Identity: 87.578

alignment_block:

US-09-218-277-12 x MUSMBP78M ..

Align seg 1/1 to: MUSMBP78M from: 1 to: 1939

13 SerLysTyrLeuAlaThrAlaSerThrMetAspHisAlaArgHisGlyPhe 29

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6 TCCAAAGTACCTGGCCACAGCAAGTACCATGGACCATGCCAGGCATGGCTT 55

|||||

29 eLeuProArgHisArgAspThrGlyIleLeuAspSerIleGlyArgPheP 46

|||||

56 CCTCCCAAGGCACAGACACGGGCATCCTTGACTCCATCGGGCGCTTCT 105

|||||

46 heGlyGlyAspArgGlyAlaProLysArgGlySerGlyLysAspSerHis 62

|||||

106 TTAGCGGTGACAGGGGTGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC 155

|||||

63 HisProAlaArgThrAlaHisTyrGlySerLeuProGlnLysSer....H1 78

|||||

156ACGAGAAGTACCATATATGGCTCCCTGCCCAAGAGTGCACGA 199

|||||

78 sGlyArgThrGlnAspGluAsnProValValHisPhePheLysAsnIleV 95

|||||

200 CGCGCGGACCCCAAGATGAARACCCAGTAGTCCATTCTTCAAGACATG 249

|||||

95 alThrProArgThrProProSerGlnGlyLysGlyArgGlyLeuSer 111

|||||

250 TGACACCTCGAACACCACTCCATCCATCCCAAGGAAG..... 284

|||||

112 LeuSerArgPheSerTrpGlyAlaGluGlyGlnArgProGlyPheGlyTy 128

|||||

285GGGGCCGAGGGGCGAAGCCAGGATTGGCTA 316

|||||

128 rGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGlyPheLysGlyV 145

|||||

317 CGGAGGCGAGGCTTCGACATATAATCGGCTCACAGGGGATTCAAGGGG 366

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145 al...AspAlaGlnGlyThrLeuSerLysLysIlePheLysLeuGlyArg 160

|||||

367 CCTACGACGCCAGGGCAGCCTTCCAAAATCTTTAAGCTGGGAGGAAGA 416

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161 AspSerArgSerGlySerProMetAlaArgArg 171

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417 GACAGCGCTCTGGATCTCCCATGGCGAGACGC 449

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seq_name: gb_ro:RATMBP2A

seq_documentation_block:

LOCUS RATMBP2A 612 bp mRNA ROD 27-APR-1993

DEFINITION Rat myelin basic protein mRNA, complete cds.

ACCESSION M25889

VERSION M25889.1 GI:205321

KEYWORDS myelin basic protein.

SOURCE Rat (18-day old) brain, cDNA to mRNA, clone pMBP2.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 612)

AUTHORS Schaich,M., Budzinski,R.-M. and Stoffel,W.

TITLE Cloned proteolipid protein and myelin basic pritein cDNA:

Transcription of the two genes during myelination

Biol. Chem. Hoppe-Seyler 367, 825-834 (1986)

JOURNAL MEDLINE

87026249

FEATURES

Source

1..612

/organism="Rattus norvegicus"

/db_xref="taxon:10116"

41..427

/note="myelin basic protein"

/codon_start=1

/protein_id="AAA41575.1"

/db_xref="GI:205322"

/translation="MASQRFSQRHGSKYLATASTMDHARHGFLPRHRDGTGILDSIGR

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KRGSLSRFSWGGDRSRSGSPMARR"

BASE COUNT 151 a 195 c 148 g 118 t

ORIGIN

alignment_scores:

Quality: 615.50 Length: 171

Ratio: 4.809 Gaps: 3

Percent Similarity: 74.854 Percent Identity: 72.515

alignment_block:

US-09-218-277-12 x RATMBP2A ..

Align seg 1/1 to: RATMBP2A from: 1 to: 612

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17

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41 ATGCATCATCAGACAGAGACCCCTCACAGCGACACGGATCCCAAGTACTTGGC 90

|||||

17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34

|||||

91 CACAGCAAGTACCATGGACCATGCCCGGCATGGCTTCTCCCAAGGCACA 140

|||||

34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50

|||||

141 GAGACAGCGGCATCCTTACTCCATCGGGCGCTTCTTAGCGGTGACAGG 190

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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67

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191 GGTGGCCCAAGCGGGCTCTGGCAAGGACTCACAC.....ACAAGAAC 234
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
   ::::::::::::::::::::::::::::::::::::
235 TACCCACATACGCTCCCTGCCCAAGATCGCAG...AGGACCCCAAGATG 281
84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
   ::::::::::::::::::::::::::::::::::::::
282 AAAACCCAGTAGTCCACTCTTCAGACACATGTGACACCTCGTACACCC 331
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
   ::::::::::::::::::::::::::::::::::::::
332 CTTCCATCCCAAGGAAGGGAGAGCGCTGTCCCTCAGCAGATTTAGCTG 381
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSerA 134
   |
382 G..... 382
134 spTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
382 ..... 382
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
   ::::::::::::::::::::::::::::::::::::::
383 ..... 411
167 oMetAlaArgArg 171
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412 CATGGCAAGACGC 424

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seq_name: gb_ro:RNO132895

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seq_documentation_block:
LOCUS      RNO132895      387 bp      mRNA      ROD      11-FEB-1999
DEFINITION Rattus norvegicus mRNA for myelin basic protein, 14kDa isoform.
ACCESSION  AJ132895
VERSION    AJ132895.1 GI:4454310
KEYWORDS   isoform; mbp gene; myelin; myelin basic protein.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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REFERENCE  1 (bases 1 to 387)
AUTHORS   Lobell,A.M.
TITLE     Direct Submission
JOURNAL   Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
            Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
            SWEDEN
REFERENCE  2 (bases 1 to 387)
AUTHORS   Lobell,A.M. and Wigzell,H.
JOURNAL   Unpublished
FEATURES   Location/Qualifiers
            source
              1..387
                /organism="Rattus norvegicus"
                /strain="Lewis rat"
                /db_xref="taxon:10116"
            gene
              1..387
            CDS
              1..387
                /gene="mbp"
                /note="14kDa isoform"
                /codon_start=1
                /product="myelin basic protein"
                /protein_id="CAA10804.1"
                /db_xref="GI:4454311"
                /translation="MASQKRPDSRHGSKYLATASMDHARGFLPRHRDGIILDSIGR
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            BASE COUNT      103 a      124 c      99 g      61 t
            ORIGIN

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alignment_scores:

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Quality: 611.50      Length: 171
Ratio: 4.777      Gaps: 3
Percent Similarity: 74.854      Percent Identity: 71.930

alignment_block:
US-09-218-277-12 x RNO132895 ..
Align seg 1/1 to: RNO132895 from: 1 to: 387

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
   ::::::::::::::::::::::::::::::::::::::
1 ATGCATCACAGAAGAGACCCCTCACAGCGACGATCCCAAGTACTTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
   ::::::::::::::::::::::::::::::::::::::
51 CACAGCAAGTACCATGGACATGCCGGCATGGCTCTCCCAAGGCACA 100
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
   ::::::::::::::::::::::::::::::::::::::
101 GAGACACGGGCATCTTGACTCCATCGGGCGCTTCTTAGCGGTGACAGG 150
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
   ::::::::::::::::::::::::::::::::::::::
151 GGTGGCCCAAGCGGGCTCTGGCAAGGACTCACAC.....ACAAGAAC 194
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
   ::::::::::::::::::::::::::::::::::::::
195 TACCCACTACGCTCCCTGCCCAAGATCGCAG...AGGACCCCAAGATG 241
84 luAsnProValValHisPheLysAsnIleValThrProArgThrPro 100
   ::::::::::::::::::::::::::::::::::::::
242 AAAACCCAGTAGTCCACTCTTCAGACACATGTGACACCTCGTACACCC 291
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
   ::::::::::::::::::::::::::::::::::::::
292 CTTCCATCCCAAGGAAGGGAGAGCGCTGTCCCTCAGCAGATTTAGCTG 341
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSerA 134
   |
342 G..... 342
134 spTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
342 ..... 342
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
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343 ..... 371
167 oMetAlaArgArg 171
   ::::::::::::::
372 CATAGCAAGACGC 384

seq_name: gb_ro:RATMBP
seq_documentation_block:
LOCUS      RATMBP      1464 bp      mRNA      ROD      27-APR-1993
DEFINITION rat myelin basic protein (mbp) gene mRNA.
ACCESSION  K00512
VERSION    K00512.1 GI:205320
KEYWORDS   .
SOURCE     rat (sprague dawley, newborn) cdna to brain mrna.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE  1 (bases 1 to 1464)
AUTHORS   Roach,A., Boylan,K.B., Horvath,S., Prusiner,S.B. and Hood,L.E.
TITLE     Characterization of cloned cdna representing rat myelin basic
            protein: absence of expression in brain of shiverer mutant mice
            Cell 34, 799-806 (1983)
JOURNAL   MEDLINE 84026484
COMMENT    mbp's have been found in rats, small (m-r=14,000) and large
            (m-r=18,500). the sequence shown is for the small mbp, however the

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authors do not rule out one gene for both proteins.

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FEATURES             source
    Location/Qualifiers
     i..1464
    /organism="Rattus norvegicus"
    /db_xref="taxon:10116"
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...
alignment_scores:
  Quality: 611.50      Length: 171
  Ratio: 4.777        Gaps: 3
  Percent Similarity: 74.854  Percent Identity: 71.930
alignment_block:
US-09-218-277-12 x RATMBP ..
Align seg 1/1 to: RATMBP from: 1 to: 1464
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25 ATGGCATCAGAGAGAGACCTCACAGCAGACGGATCCAAGTACTTGGC 74
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
75 CACAGCAAGTACCATTGACCATGACCATGCCCGCATGGCTTCTCCCAAGGCACA 124
|||||
34 rGaspThrGlyLeuLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
125 GAGACACGGGCATCTTGACTCCATCGGGCGCTCTTTAGCGGTGACAGG 174
|||||
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProLalaArgTh 67
|||||
175 GGTGGCGCCCAAGCGGGCTCTGGCAAGGACTCACAC.....ACAAGAAC 218.
|||||
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
219 TACCACATCGGCTCCCTGCCCAAGAGTCGCAG...AGGACCCCAAGATG 265
|||||
84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
|||||
266 AAAACCCAGTAGTCCACTTCTTCAAGAACATTTGACACCTCGTACACC 315
|||||
101 ProProSerGlnGlyLysArgGlyLeuSerLeuSerArgPheSerTr 117
|||||
316 CCTCCATCCCAAGGAAGAGGAGAGGCGCTGCCCTCAGCAGATTAGCTG 365
|||||
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
|||||
366 G..... 366
134 sPtyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
366 ..... 366
151 LeuSerLysIlePheLysLeuGlyArgAspSerArgSerGlySerPr 167
|||||
367 .....GGAGGAAGAGACAGCGCGCTCTGGATCTCC 395
167 oMetAlaArgArg 171
|||||
396 CATAGCAAGACGC 408
seq_name: gb_ov:GGMBP
seq_documentation_block:
LOCUS GGMBP 2256 bp mRNA VRT 12-SEP-1993
DEFINITION Chicken mRNA for myelin basic protein.
ACCESSION X17103
VERSION X17103.1 GI:63594
KEYWORDS myelin basic protein.
SOURCE chicken.
ORGANISM Gallus gallus

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Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 2256)
Gundelfinger,E.D.
Direct Submission
Submitted (08-NOV-1989) Gundelfinger E. D., Universitaet Hamburg,
Universitaetskrankehaus Eppendorf, Zentrum fuer Molekulare
Neurobiologie, Martinistrasse 52, 2000 Hamburg 20, FRG
2 (bases 1 to 2256)
Zopf,D., Sonntag,V., Betz,H. and Gundelfinger,E.D.
Developmental accumulation and heterogeneity of myelin basic
protein transcripts in the chick visual system
Glia 2 (4), 241-249 (1989)
MEDLINE
89358239
FEATURES             source
    Location/Qualifiers
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    /strain="white leghorn"
    /db_xref="taxon:9031"
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    /tissue_type="brain optic lobe"
    /cell_type="oligodendrocytes"
    /clone_lib="lambda gt10"
    /clone="0219/10, 0219/2/3, 0219/2/2"
6..530
    /note="myelin basic protein (AA 1-174)"
    /codon_start=1
    /protein_id="CAA34959.1"
    /db_xref="GI:63595"
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SRPGSRGSGSPVAR"
misc_feature
121
    /note="sequence polymorphism"
misc_feature
318..350
    /note="splice variant"
misc_feature
892..897
    /note="polyA signal"
misc_feature
912
    /note="processing variant"
misc_feature
1719
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misc_feature
1812
    /note="sequence polymorphism"
misc_feature
2234..2239
    /note="polyA signal"
BASE COUNT      666 a   486 c   465 g   639 t
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alignment_scores:
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  Ratio: 4.050        Gaps: 7
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US-09-218-277-12 x GGMBP ..
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|||||
6 ATGGCTTCACAAAACGCTCCTCTTCCGCGCAGGATCAAA...ATGCG 52
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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
53 ATCGCAAGCACTACAGACACTGCTCGACATGGA...TCTCCAAGGCACA 99
|||||
34 rGaspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
100 GAGACTCGGGTCTACTTGACTCTCTGGCGAGATTCTTTGGAGGTGACAGA 149

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51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
150 CACGTCCTCCCGGGGGCTTTGGCAGGATATA...CAGCGAGCCAGGCG 196
67 rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGlnA 83
197 CAGCCATGTAGGCTCCATCCCCCAGAGGTCTCAGCATGCGCGCTGGTG 246
83 sPLuAsnProValValHisPhePheLysAsnIleValThrProArgThr 99
247 AGGACAACCTCTAGTCACCTCTTCAAGACATCTCTCACCCTGACT 296
100 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSe 116
297 CTCTCTCCATCAAGCAAGGAGAGGACTGTCTCTCACCAGATTAG 346
116 rTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAla 133
347 CTGGGTGGTGAAGGACACACAGCGGATACGGA...AGTGGAAATTC 393
133 eAspTyrLysSerAlaHisLysGlyPheLysGlyVal.....AspAla 147
394 ATGAGCACAAATCTGCTCACAAAGGACACAGAGGATCTCTATCACGAG 443
148 GlnGlyThrLeuSerLysLysPheLysLeuGlyGlyArg..... 160
444 CAGGACACTCTTTCCAAATCTTTAACTGGGAGGCTGTGGTCCCGGCC 493
161 AspSerArgSerGlySerProMetAlaArgArg 171
494 TGGATCGCGGCTGTGGCTCACCATGTTGCGAGGCGC 527

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seq_name: gb_ro:RNO132896

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seq_documentation_block:
LOCUS      RNO132896      465 bp      mRNA      ROD      11-FEB-1999
DEFINITION Rattus norvegicus mRNA for myelin basic protein, 17 kDa isoform.
ACCESSION  AJ132896
VERSION    AJ132896.1  GI:4454312
KEYWORDS   isoform; mbp gene; myelin; myelin basic protein.
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
REFERENCE  1 (bases 1 to 465)
AUTHORS   Lobell,A.M.
TITLE     Direct Submission
JOURNAL   Submitted (09-FEB-1999) Lobell A.M., Karolinska Institute,
            Microbiology and Tumorbiology Center, Box 280, 171 77 Stockholm,
            SWEDEN
REFERENCE  2 (bases 1 to 465)
AUTHORS   Lobell,A.M. and Wigzell,H.
JOURNAL   Unpublished
FEATURES   Location/Qualifiers
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                        /strain="Lewis rat"
                        /db_xref="taxon:10116"
            gene            1..465
                        /gene="mbp"
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                        /note="17 kDa isoform"
                        /codon_start=1
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                        /protein_id="CAA10805.1"
                        /db_xref="GI:4454313"
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                        RTQDENPVWHFFKNIVTPRTPPPSQSGKRGLSLRSFSWGGDRSRSQSPIARR"
BASE COUNT  117 a 153 c 120 g 75 t
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    Ratio: 4.598        Gaps: 4
    Percent Similarity: 64.975    Percent Identity: 62.437

alignment_block:
US-09-218-277-12 x RNO132896 ..
Align seg 1/1 to: RNO132896 from: 1 to: 465

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1  ATGGGATCACAGAGAGACCTTCACAGGCACAGGATCCAAAGTACTTGGC 50
17  aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51  CACAGCAAGTACCATTGGACCATGCCCGCATGGCTTCCTCCCAAGGCACA 100
34  rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
101  GAGACACGGGATCCTTGACTCCATCGGCGCTTCTTTAGCGGTGACAGG 150
51  GlyAlaProLysArgGlySerGly..... 58
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151  GTTGGCCCCAAGCGGGGCTCTGGCAAGGTACCTGGCTAAAGCAGAGCGG 200
58  ..... 58
201  GAGCCCTCTGCTTCTCATGCCGAGCGCTCCCGGGCTGTGCCACATGT 250
59  ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
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251  ACAGGACTCACAC.....ACAAGACTAGCCACTACGGCTCCCTGCC 294
75  GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
|||||
295  CAGAAAGTCGCGAG...AGGACCCCAAGATGAAACCCAGTAGTCCACTTCT 341
91  eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
|||||
342  CAAGAACAATGTGCACACTCGTACACCCCTCCATCCCAAGGAAGGGA 391
108  rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
|||||
392  GAGGCTGTCCCTCAGCAGATTTAGCTGG..... 420
125  GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysGl 141
420  ..... 420
141  yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
421  .....G 421
158  lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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422  GAGGAAGAGACAGCGGCTCTGGATCTCCCATAGCAAGACGC 462

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251 AAAACCCCGTAGTCCACTTCTTCAAGAACATTGTGACGCCCTCGCACACCA 300

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101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
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301 CCCCGTCGACGGAAGAGGAGGAGGACTGCTCCCTGAGCAGATTAGCTG 350
|||||
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
|||||
351 GGGGCCCAAGCCAGACAGCAGGATTTGGCTACGGAGGCAGAGCGTCCG 400
|||||
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
|||||
401 ACTATAATCGCTGCACAAAGGATTCAGAGGAGTCGATGCCAGGCGACG 450
|||||
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
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167 oMetAlaArgArg 171
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501 CATGGCTAGACGC 513

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seq_name: N_Geneseq_36:T32561

seq_documentation_block:

ID T32561 standard; DNA; 516 BP.

AC T32561;

DT 07-NOV-1996 (first entry)

DE Human myelin basic protein (MBP) coding sequence.

KW Myelin basic protein; MBP; multiple sclerosis; MS; competition;

KW inhibition; major histocompatibility complex; MHC; thymocyte; T cell;

KW experimental allergic encephalomyelitis; EAE; analogue; treatment;

KW prevention; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT cds 1..516

FT /*tag- a

FT /product= Myelin basic protein.

PN W09616086-A1.

PD 30-MAY-1996.

PF 16-NOV-1995; U14403.

PR 18-NOV-1994; US-342408.

PA (NEUR-) NEUROCRINE BIOSCIENCES INC.

PI Conlon PJ, Gaur A, Ling N, Steinman L;

DR WPI; 96-268535/27.

DR P-PSDB; R99580.

PT Peptide analogues of human myelin basic protein - useful for

PT treatment of multiple sclerosis

PS Disclosure; Figure 1: 61pp; English.

CC Peptide analogues comprising at least seven amino acids from

CC residues 86-99 of human myelin basic protein (MBP), can be used to

CC treat multiple sclerosis by competing for the binding of native MBP

CC peptide to MHC and by not causing proliferation of an MBP reactive T-

CC cell line. The peptide analogues also inhibit the induction of

CC experimental allergic encephalomyelitis (EAE) by MBP in rodents.

CC The peptide analogues have a reduced susceptibility to proteolysis

CC in vivo.

SQ Sequence 516 BP; 130 A; 153 C; 149 G; 84 T;

alignment_scores:

Quality: 922.00 Length: 171

Ratio: 5.392 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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|||||

1 ATGGCGTCACAGAGAGACCTCCAGAGGCACGGATCCCAAGTACCTGGC 50

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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34

|||||

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|||||
51 CACAGCAAGTACCATTGACCATGCCAGGCTGCTCTCCCAAGGCACA 100
|||||
34 rgAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
|||||
101 GAGACAGGGCATCCTTGACTCCATCGGGCGCTTCTTTGGCGGTGACAGG 150
|||||
51 GlyAlaProLysArgGlySerGlyLysAspSerHisHisProAlaArgTh 67
|||||
151 GGTGCGCAAAAGCGGGCTCTGGCAAGGACTCACACCACCGGCAAGAAC 200
|||||
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84
|||||
201 TGTCTACTATGGCTCCCTGCCCAAGAGTACACACGCGCGGACCAAGATG 250
|||||
84 luAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
|||||
251 AAAACCCCGTAGTCCACTTCTTCAAGAACATTGTGACGCCCTCGACACCA 300
|||||
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
|||||
301 CCCCGTCGACGGAAGAGGAGGAGGACTGCTCCCTGAGCAGATTAGCTG 350
|||||
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyGlyArgAlaSerA 134
|||||
351 GGGGCCCAAGCCAGACAGCAGGATTTGGCTACGGAGGCAGAGCGTCCG 400
|||||
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
|||||
401 ACTATAATCGCTGCACAAAGGATTCAGAGGAGTCGATGCCAGGCGACG 450
|||||
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
|||||
451 CTTTCCAAATTTTAAGCTGGGAGGAAGATAGTCGCTCTGGATCACC 500
|||||
167 oMetAlaArgArg 171
|||||
501 CATGGCTAGACGC 513

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seq_name: N_Geneseq_36:T41889

seq_documentation_block:

ID T41889 standard; cDNA to mRNA; 594 BP.

AC T41889;

DT 01-FEB-1997 (first entry)

DE Human myelin basic protein (foetal isoform) cDNA.

KW Myelin basic protein; MBP; MBP-X2Cys81; proteolipid protein;

KW PLP; multiple sclerosis; MBP; autoimmune disease; diagnosis; therapy;

KW T-lymphocyte; T-cell; anergy; apoptosis; ds.

OS Homo sapiens.

PN W09634622-A1.

PD 07-NOV-1996.

PF 22-APR-1996; U05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Peifrey CW, Squinto SP, Wilkins JA;

DR WPI; 96-503898/50.

DR P-PSDB; W00399.

PT New human myelin basic protein and proteolipid protein variant(s) -

PT used in the assessment, diagnosis and treatment of multiple

PT sclerosis

PS Claim 6; Page 79-80; 156pp; English.

CC A cDNA sequence (T41889) codes for the native human 21.5 kDa foetal

CC isoform (W00399) of myelin basic protein, MBP-X2Cys81/hum. This

CC isoform includes an exon 2-encoded region (X2) that may contain an

CC epitope involved in the pathogenesis of multiple sclerosis (MS); the

CC X2 region is not found in the MBP of healthy adults. The cDNA can be

CC obtd. by PCR amplification (see also T42785-90) and used to produce

CC recombinant MBP 21.5 in host, pref. bacterial, cells (see also

CC T41896-97). Recombinant MBP 21.5 polypeptides are useful in the
 CC clinical assessment, diagnosis and treatment of MS. 96 T;
 SQ Sequence 594 BP; 143 A; 184 C; 171 G; 96 T;

alignment_scores:
 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:
 US-09-218-277-12 x T41889 ..

Align seg 1/1 to: T41889 from: 1 to: 594

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1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
1 ATGGCGTCAAGAGAGACCTCCAGAGGCACGGATCCAAAGTACCTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHis 34
|||||
51 CACAGCAAGTACATGACCATGCCAGGATGCTTCCTCCCAAGGCACA 100
34 rgAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
|||||
101 GAGACACGGGCATCCTTGACTCATCGGGCGCTTCTTTGGCGGTGACAG 150
51 GlyAlaProLysArgGlySerGly..... 58
151 GGTGGCCCCAAGCGGGCTCTGGCAAGGTACCTGTGCTAAAGCGGGCGC 200
58 ..... 58
201 GAGCCCTCTGCCCTCTATGCGCGCAGCGCCTGGGCTGTGCAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGGACTCACACACCGCGGCAAGACTGCTCACTATGGTCCCTGGCC 300
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
301 CAGAAGTCACACGGCGGCGGCCCAAGATGAAACCCCGTAGTCCACTTCT 350
91 elysasnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
351 CAAGAACAATTGTACCCCTCGCACACACCCCGCTCGCAGGGAAAGGGA 400
108 rgGlyLeuSerLeuSerArgPheSerTyrGlyAlaGluGlyGlnArgPro 124
401 GAGGACTGTCCCTGACACATTTAGTGGGGGCCGCAAGCCAGAGACCA 450
125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLys 141
451 GGATTGGCTAGCGAGGACAGCGTCCGACTATATAATCGGTCACAAAGG 500
141 yPheLysGlyValAspAlaGlnClyThrLeuSerLysIlePheLysLeu 158
501 ATTCAAGGAGATGATGCGCCAGGGCAGCTTTCCAAAATTTTCAAGCTG 550
158 lyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
551 GAGGAAGAGATAGTCTGCTCGATCACCCATGCTGCTAGACGC 591

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seq_name: N_Geneseq_36:T41896

seq_documentation_block:

ID T41896 standard; DNA; 612 BP.
 AC T41896;
 DT 01-FEB-1997 (first entry)
 DE Fetal myelin basic protein MBP+X2Cys81/bact. DNA.
 KW Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
 KW multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis; ds.

OS Synthetic.
 PN W09634622-A1.
 PD 07-NOV-1996. U05611.
 PF 22-APR-1996; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pellfrey CM, Squinto SP, Wilkins JA;
 DR WPI; 96-505898/50.
 DR P-PSDB: W06107.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Disclosure; Page 81-82; 156pp; English.
 CC A DNA sequence (T41896) codes for the human 21.5 kDa foetal isoform
 CC (W06107) of myelin basic protein, MBP+X2Cys81/bact., and utilises
 CC bacterially-preferred codons in place of the native human codons
 CC (see also T41889). This increases prodn. of the MBP in E. coli by
 CC at least 50%. Recombinant MBP 21.5 polypeptides (see also W00399
 CC and W06108) are useful in the clinical assessment, diagnosis and
 CC treatment of MS.
 SQ Sequence 612 BP; 117 A; 215 C; 166 G; 114 T;

alignment_scores:
 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:

US-09-218-277-12 x T41896 ..

Align seg 1/1 to: T41896 from: 1 to: 612

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1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
1 ATGGCGTCTCAGAAACGTCCTCCGAGGTCACGGCTCCAAATACCTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHis 34
51 CACCGCCAGCACCATGGACCATGCCGCTCATGCTCTCTCGCGCGTACCC 100
34 rgAspThrGlyIleLeuAspSerIleGlyArgPheGlyGlyAspArg 50
101 GTGACACGGGCATCCTGGACTCCATCGCGCGCTTCTTCGGCGGTGACCG 150
51 GlyAlaProLysArgGlySerGly..... 58
151 GGTGGCGCCGAAACGTCGCTCTGGCAAGTGCCTGGCTGAAACCGGGCGC 200
58 ..... 58
201 TAGCCCGCTGCCGTCTCATGCCCGTAGCCGCGCGGCTGTGCACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGACTCCCAACACCGCGCTCGTACCGGCACATATGGCTCCCTGGCC 300
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
301 CAGAAATCCACGGCGGTATCCAGGATGAAACCCCGGTGGTGGCTTCTT 350
91 elysasnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
351 CAAAACATTTGTACCCCGCTACCCCGCGCTCTCAGGGCAAGGCC 400
108 rgGlyLeuSerLeuSerArgPheSerTyrGlyAlaGluGlyGlnArgPro 124
401 GTGGCGCTGTCCCTGAGCCCTTTAGCTGGGGCGCGCAAGGCCAGCGTCCG 450

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125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 451 GCCTTCGGTTACGGCGCGCTGCGTCCGACTATAAATCTGCTCACAAGG 500
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysLysIlePheLysLeuG 158
 501 CTTCAAGGCGTGGATGCCAGGCTACCTTGTCCAAAATTTTCAAACTGG 550
 158 LyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
 551 GCGGCGGTATACCGCTTCGTGGCTCTCCGATGCTAGACGT 591

seq_name: N_Geneseq_36:T41897

seq_documentation_block:
 ID T41897 standard; DNA; 612 BP.
 AC T41897;
 DT 01-FEB-1997 (first entry)
 DE Foetal myelin basic protein MBP-X2Ser81/bact.
 KW Myelin basic protein; MBP; MBP-X2Ser91; proteolipid protein; PLP;
 KW Multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KW T-lymphocyte; T-cell; anergy; apoptosis; ds.
 OS Synthetic.
 PN W09634622-Al.
 PD 07-NOV-1996.
 PF 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PR (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI: 96-505898/50.
 DR P-PSDB: W06108.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Disclosure: Page 82-83; 156pp; English.
 CC A DNA sequence (T41897) codes for the human 21.5 kDa foetal isoform
 CC (W06108) of myelin basic protein, MBP-X2Ser81/bact., and utilises
 CC codons that are preferentially used in highly-expressed bacterial
 CC genes and includes a sequence coding for an N-terminal hexa-
 CC histidine tag. This facilitates large-scale prodn. and purification
 CC of MBP 21.5 polypeptide in bacterial host cells. Recombinant MBP
 CC 21.5 polypeptides (see also W00399 and W06107) are useful in the
 CC clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 612 BP; 117 A; 215 C; 186 G; 114 T;

alignment_scores:
 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:

us-09-218-277-12 x T41897 ..

Align seg 1/1 to: T41897 from: 1 to: 612

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
 1 ATGCGGCTCAGAAACGCTCGCTCCAGCGTCACGGCTCCAAATACCTGGC 50
 17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
 51 CACCGCCAGACCATGACCATGCCCTCATGGCTTCCTGCCGGCTCACC 100
 34 rGaspThrGlyIleLeuAspSerIleGlyArgPhePheGlyLysArg 50
 101 GTGACACCGGCATCCTGGACTCCATCGCGCGCTTCCTTCGGCGGTGACCGT 150
 51 GlyAlaProLysArgGlySerGly..... 58

151 GGTGCGCCGAAACGTGGCTCTGCAAAAGTGCCTGGCTGAAACCGGGCGG 200
 58 58
 201 TAGCCCGCTGCGCGTCTCATGCCGCTAGCCAGCGGGCGCTGTGCAACATGT 250
 59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
 251 ACAAGACATCCACACCGCGCTGCTACCGCGCACTATGCTGCTCCCTGCGG 300
 75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
 301 CAGAAATCCACGCGCGTACCAGGATGAAACCCCGTGGTGCATCTCTT 350
 91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
 351 CAAAAACATTGTGACCCCGCTACCCCGCGCGCTCTCAGGGCAAGGCC 400
 108 rGlyLeuSerLeuSerArgPheSerTyrGlyAlaGluGlyGlnArgPro 124
 401 GTGGCTGTCCCTGAGCGCTTCAGCTGGGCGCGCAAGCCAGCGTCCG 450
 125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 451 GGCTTCGGTTACGGCGCGCTGCTCCGACTATAAATCTGCTCACAAGG 500
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysLysIlePheLysLeuG 158
 501 CTTCAAGGCGTGGATGCCAGGCTACCTTGTCCAAAATTTTCAAACTGG 550
 158 LyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
 551 GCGGCGGTATACCGCTTCGTGGCTCTCCGATGCTAGACGT 591

seq_name: N_Geneseq_36:T41893

seq_documentation_block:

ID T41893 standard; DNA; 1122 BP.

AC T41893;
 DT 01-FEB-1997 (first entry)
 DE MP4 chimera (MBP21.5-delta PLP4 fusion) DNA.
 KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;
 KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KW therapy; T-lymphocyte; T-cell; MP4 chimera; ds.
 OS Synthetic.
 PN W09634622-Al.
 PD 07-NOV-1996.
 PF 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PR (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI: 96-505898/50.
 DR P-PSDB: W06103.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 46; Page 110-112; 156pp; English.
 CC A DNA construct (T41893) codes for MP4 chimera (W06103), a fusion
 CC protein composed of human myelin basic protein (MBP) foetal isoform
 CC MBP21.5 (see also W00399) and delta PLP4 (W06101), a proteolipid
 CC protein (PLP) mutein that lacks all 4 hydrophobic domains of
 CC native human PLP (W06106) but includes PLP epitopes associated with
 CC multiple sclerosis (MS). It was constructed from DNA sequences
 CC encoding MBP21.5 (T41889) and delta PLP4 (T41891). The gene fusion
 CC in vector pMT22b was used to express MP4 in E. coli W3110 (DE3).
 CC PLP polypeptides (see also W00400, W06101-02 and W06104-05) can be
 CC used in the clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 1122 BP; 241 A; 354 C; 296 G; 231 T;

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alignment_scores:
  Quality: 899.00      Length: 197
  Ratio: 5.257         Gaps: 1
  Percent Similarity: 86.802  Percent Identity: 86.802

alignment_block:
US-09-218-277-12 x T41893 ..

  Align seg 1/1 to: T41893 from: 1 to: 1122

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
1 ATGGCGTCTCAGAACGTCCTCCAGCGTCACGGCTCCAAATACCTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
51 CACCGCCAGCAGCACCATTGGACCATGCCCGTCATGGCTTCTGCGCGTCACC 100
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
101 GTGACACCGGATCTGTGACCTCCATCGCGCTTCCTTCGGCGGTGACCGT 150
51 GlyAlaProLysArgGlySerGly..... 58
151 GGTGCGCGGAACGTCGTCTGGCAAGTGCCTGGTGAACCGGGCCG 200
58 ..... 58
201 TAGCCCGCTGCCGTCTCATGCCCGTAGCCAGCGCGCTGTGCAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGAGACTCCACACCCGCGCTCGTACCGCGCATTGCTGCTCCCTGCCG 300
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
301 CAGAAATCCACACGCGCTACCCAGGATGAAACCCCGGTGGTGCACCTTCTT 350
91 eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGlyA 108
351 CAAAAACATTGTGACCCCGCGTACCCCGCGCGCTCTCAGGGCAAGGCC 400
108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
401 GTGCGCTGTCCCTGAGCGGTTTCAGCTGGGCGCGCGAAGCGCAGCGTCG 450
125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
451 GCGTTCGGTTACGGCGCGCGTGGTCCGACATATAATCTGCTCACAAGG 500
141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
501 CTTCAAGCGCTGGATGCCAGGTACCTTGTCCAAATTTTCAACATGG 550
158 lyGlyArgAspSerArgSerGlySerProMetAlaArg 171
551 CGGCGCGTGATAGCGGTTCTGGCTCTCGGATGGGTAGACGT 591

seq_name: N_Geneseq_36.T41892

seq_documentation_block:
ID T41892 standard; DNA; 1155 BP.
AC T41892;
DT 01-FEB-1997 (first entry)
DE MP3 chimera (MBP21.5-delta PLP3 fusion) DNA.
KW Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
KW therapy; T-lymphocyte; T-cell; MP3 chimera; ds.
OS Synthetic.
PN WO9634622-A1.
PD 07-NOV-1996.

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PF 22-APR-1996; U05611.
PR 02-MAY-1995; US-431648.
PR 02-MAY-1995; US-431644.
PR 07-JUN-1995; US-482114.
PA (ALEX-) ALEXION PHARM INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Lenardo MJ, Matlis L, McFarland HF, Mueller EE, Mueller JP;
PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
DR WPI; 96-505898/50.
DR P-PSDB; W06102.
PT New human myelin basic protein and proteolipid protein variant(s) -
PT used in the assessment, diagnosis and treatment of multiple
PT sclerosis
PS Claim 45; Page 108-110; 156pp; English.
CC A DNA construct (T41892) codes for MP3 chimera (W06102), a fusion
CC protein composed of human myelin basic protein (MBP) foetal isoform
CC MBP21.5 (see also W00399) and delta PLP3 (W00400), a proteolipid
CC protein (PLP) mutein that lacks hydrophobic domains 1, 3 and 4 of
CC native human PLP (W06106) but includes PLP epitopes associated with
CC multiple sclerosis (MS). It was constructed from DNA sequences
CC encoding MBP21.5 (T41889) and delta PLP3 (T41890). The gene fusion
CC in vector pET22b was used to express MP3 in E. coli W3110 (DE3).
CC PLP polypeptides (see also W00400, W06101 and W06103-05) can be
CC used in the clinical assessment, diagnosis and treatment of MS.
SQ Sequence 1155 BP; 239 A; 363 C; 306 G; 247 T;

alignment_scores:
 Quality: 899.00 Length: 197
 Ratio: 5.257 Gaps: 1
 Percent Similarity: 86.802 Percent Identity: 86.802

alignment_block:
US-09-218-277-12 x T41892 ..

Align seg 1/1 to: T41892 from: 1 to: 1155

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
1 ATGGCGTCTCAGAAACGTCGCTCCAGCGTCACGGCTCCAAATACCTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
51 CACCGCCAGCAGCACCATTGGACCATGCCCGTCATGGCTTCTTCGGCGGTGACCG 100
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
101 GTGACACCGGATCTGTGACCTCCATCGCGCTTCCTTCGGCGGTGACCGT 150
51 GlyAlaProLysArgGlySerGly..... 58
151 GGTGCGCGGAACGTCGTCTGGCAAGTGCCTGGTGAACCGGGCCG 200
58 58
201 TAGCCCGCTGCCGTCTCATGCCCGTAGCCAGCGCGCTGTGCAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGAGACTCCACACCCGCGCTCGTACCGCGCATTGCTGCTCCCTGCCG 300
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValValHisPhePh 91
301 CAGAAATCCACACGCGCTACCCAGGATGAAACCCCGGTGGTGCACCTTCTT 350
91 eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGlyA 108
351 CAAAAACATTGTGACCCCGCGTACCCCGCGCGCTCTCAGGGCAAGGCC 400
108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
401 GTGCGCTGTCCCTGAGCGGTTTCAGCTGGGCGCGCGAAGCGCAGCGTCG 450
125 GlyPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
451 GCGTTCGGTTACGGCGCGCGTGGTCCGACATATAATCTGCTCACAAGG 500
141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
501 CTTCAAGCGCTGGATGCCAGGTACCTTGTCCAAATTTTCAACATGG 550
158 lyGlyArgAspSerArgSerGlySerProMetAlaArg 171
551 CGGCGCGTGATAGCGGTTCTGGCTCTCGGATGGGTAGACGT 591

seq_name: N_Geneseq_36.T41892

seq_documentation_block:
ID T41892 standard; DNA; 1155 BP.
AC T41892;
DT 01-FEB-1997 (first entry)
DE MP3 chimera (MBP21.5-delta PLP3 fusion) DNA.
KW Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;
KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
KW therapy; T-lymphocyte; T-cell; MP3 chimera; ds.
OS Synthetic.
PN WO9634622-A1.
PD 07-NOV-1996.

125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 |||||
 451 GCGTTCGGTTACGGCGCGCGTGGCTCGACTATAAATCTGCTCACAAAG 500
 |||||
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
 |||||
 501 CTTCAAGGCGTGGATGCCAGGGTACCTGTGCCAAAATTTTCAAACTGG 550
 |||||
 158 lyGlyArgAspSerArgSerGlySerProMetAlaArg 171
 |||||
 551 GCGGCGGTGATACCGCTTCTGGCTCTCCGATGGCTAGACGT 591
 |||||

seq_name: N_Geneseq_36:T41895

seq_documentation_block:

ID T41895 standard; DNA; 1476 BP.

AC T41895;

DT 01-FEB-1997 (first entry)

DE MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion) DNA.

KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

KW therapy; T-lymphocyte; T-cell; MMOGP4 chimera;

KW myelin oligodendrocyte glycoprotein; MOG; ds.

OS Synthetic.

PN W09634622-A1.

PD 07-NOV-1996.

PF 22-APR-1996; U05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

PI WPI; 96-505898/50.

DR P-PSDB; W06105.

PT New human myelin basic protein and proteolipid protein variant(s) -
 used in the assessment, diagnosis and treatment of multiple
 sclerosis

PT Claim 48;

PS Claim 115-117; 156pp; English.

CC A DNA construct (T41895) codes for MMOGP4 chimera (W06105), a fusion

protein composed of human myelin basic protein (MBP) foetal isoform

MBP21.5 (see also W00399), the extracellular domain of human myelin

oligodendrocyte glycoprotein (MOG) and delta PLP4 (W06101), a

proteolipid protein (PLP) mutin that lacks all 4 hydrophobic

domains of native human PLP (W06106) but includes PLP epitopes

associated with multiple sclerosis (MS). It was constructed by

inserting a sequence encoding the MOG moiety into MP4 chimera DNA

(see also T41893) between the MBP and PLP derived sequences. The

recombinant MMOGP4 chimera can be expressed in bacterial cell hosts.

PLP polypeptides (see also W00400, W06101-03 and W06105) are useful

in the clinical assessment, diagnosis and treatment of MS.

Sequence 1476 BP; 332 A; 434 C; 403 G; 307 T;

alignment_scores:

Quality: 899.00

Ratio: 5.257

Percent Similarity: 86.802

Percent Identity: 86.802

alignment_block:

US-09-218-277-12 x T41895 ..

Align seg 1/1 to: T41895 from: 1 to: 1476

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17

1 ATGGCGTCTCAGAAAGCTCGTCCCGAGCGTCACGGTCCAAATACCTGGC 50

17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34

1 CACCGCCAGACCATGACCATGCCCGCTCATGGCTTCTTCCGCGGTACCC 100

34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyClyAspArg 50
 |||||
 101 GTGACACCGGATCTCGACTCCATCGCGCGCTTCTTCGGCGGTGACCGT 150
 |||||
 51 GlyAlaProLysArgLysSerGly..... 58
 |||||
 151 GTGCGCGCAACAGTGGCTCTGGCAAGTGGCGTGGCTGAACACGGCGCG 200
 |||||
 58 58
 201 TAGCCCGCTGCGCTCATGCGCGTAGCCGCGGCGCTGTGCAACATGT 250
 |||||
 59 ...LysAspSerHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
 |||||
 251 ACAAGAGACTCCACCGCGCTCGTACCGCGCACTATGGCTCCCTCGCG 300
 |||||
 75 GlnLysSerHisGlyArgThrGlnAspGluProValValHisPhePh 91
 |||||
 301 CAGAATCCACCGCGCTACCCAGGATGAAACCCGCGGTGGTGCATCTCT 350
 |||||
 91 elysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
 |||||
 351 CAAAACATTGTGACCGCGTACCCGCGCGCTCTCAGGGCAAGGCC 400
 |||||
 108 rGlyLysSerLeuSerArgPheSerTrpGlyAlaGluGlyGlnArgPro 124
 |||||
 401 GTGGCTGTCTCCAGCGCTTTCAGTGGCGCGGCGGCGGCGGCGCGCG 450
 |||||
 125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG1 141
 |||||
 451 GCGTTCGGTTACGGCGCGCGTGGCTCGGCTATATAATCTGCTCAAAAGG 500
 |||||
 141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
 |||||
 501 CTTCAAGGCGTGGATGCCAGGGTACCTGTGCCAAAATTTTCAAACTGG 550
 |||||
 158 lyGlyArgAspSerArgSerGlySerProMetAlaArg 171
 |||||
 551 GCGGCGGTGATACCGCTTCTGGCTCTCCGATGGCTAGACGT 591
 |||||

seq_name: N_Geneseq_36:T41894

seq_documentation_block:

ID T41894 standard; DNA; 1125 BP.

AC T41894;

DT 01-FEB-1997 (first entry)

DE PM4 chimera (delta PLP4-MBP21.5 fusion) DNA.

KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;

KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;

KW therapy; T-lymphocyte; T-cell; PM4 chimera; ds.

OS Synthetic.

PN W09634622-A1.

PD 07-NOV-1996.

PF 22-APR-1996; U05611.

PR 02-MAY-1995; US-431648.

PR 02-MAY-1995; US-431644.

PR 07-JUN-1995; US-482114.

PA (ALEX-) ALEXION PHARM INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JP;

PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;

PI WPI; 96-505898/50.

DR P-PSDB; W06104.

PT New human myelin basic protein and proteolipid protein variant(s) -

used in the assessment, diagnosis and treatment of multiple

sclerosis

PS Claim 47; Page 113-114; 156pp; English.

CC A DNA construct (T41894) codes for PM4 chimera (W06104), a fusion

protein composed of delta PLP4 (W06101) and MBP21.5 (W00399).

CC Delta PLP4 is a proteolipid protein (PLP) mutin that lacks all 4

hydrophobic domains of native human PLP (W06106) but includes PLP

epitopes associated with multiple sclerosis (MS). MBP21.5 is a

foetal isoform of human myelin basic protein (MBP) associated with

CC MS. The DNA was constructed from sequences encoding delta PLP4
CC (T41891) and MBP21-5 (T41889). The gene fusion can be used to
CC express PM4 in bacterial hosts. PLP polypeptides (see also W00400,
CC W06101-03 and W06105) can be used in the clinical assessment,
CC diagnosis and treatment of MS.
SQ Sequence 1125 BP; 239 A; 359 C; 299 G; 228 T;

alignment_scores:
Quality: 894.00 Length: 196
Ratio: 5.259 Gaps: 1
Percent Similarity: 86.735 Percent Identity: 86.735

alignment_block:

US-09-218-277-12 x T41894 ..

Align seg 1/1 to: T41894 from: 1 to: 1125

2 AlaserGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAla18
|||||
520 GCGTCACAAAGCTCGGCCACGCTCAGGCTCCAAATACCTGGCCAC 569
18 rLaserThrMetAspHisAlaArgHisGlyPheLeuProArgHisArgA 35
|||||
570 CGCCAGCACCATGACCATGCCCGTCATGCTTCCTGCGCGGTACCGGTG 619
35 sPThrGlyLeuLeuAspSerIleGlyArgPheGlyGlyAspArgGly 51
|||||
620 ACACCGGCATCTTGACTCCATCGCGCTCTCTTCGCGGTGACCGTGTG 669
52 AlaProLysArgGlySerGly..... 58
|||||
670 GCGCCGAAAGCTGGCTCTGCAAGTGCCTGCTGCAACCGGGCGGTAG 719
59L 59
720 CCGCTGCCGTCTCATGCCGTAGCAGCGCGGCTGTGCAACATGTACA 769
59 ysAspSerHisProAlaArgThrAlaHisTyrGlySerLeuProGln 75
|||||
770 AAGACTCCACACCGCGGTCTGACCGGCACATATGCTCCCTGCGCGCAG 819
76 LysSerHisGlyArgThrGlnAspGluAspProValValHisPhePhe 92
|||||
820 AAATCCACCGCGGTACCCAGGATGAACCCGGTGTGCTCTCTCAA 869.
92 sAsnIleValThrProArgThrProProSerGlnGlyLysGlyArg 109
|||||
870 AAACATGTGACCCCGGTACCCGCGCGCTCTCAGGCAAGGCGGTG 919
109 lyLeuSerLeuSerArgPheSerTrpGlyAlaGluGlnArgProGly 125
|||||
920 GCCTGTCTCTGAGCGCTTTCAGCTGGGCGCCGAGCCAGCTCCGGGC 969
126 PheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysGly 142
|||||
970 TTCGGTACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1019
142 eLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuGly 159
|||||
1020 CAAAGCGGTGATGCCAGGCGACCTGTCCAAATTTTCAAACTGGCG 1069
159 lyArgAspSerArgSerGlySerProMetAlaArgArg 171
|||||
1070 GCGGTGATAGCTTCTGCTCTCCGATGCTGCTGCTGCTGCTGCTGCT 1107

seq_name: N_Geneseq_36:Q48976

seq_documentation_block:

ID Q48976 standard; cDNA to mRNA; 1164 BP.
AC Q48976;
DT 18-APR-1994 (first entry)
DE Nucleotides 301-1464 of rat myelin gene.

KW RB35 antigen; Immunogen; myelin; rat; brain; antibody; IgG1; ds.
OS Rattus norvegicus.
PN J05219982-A.
PD 31-AUG-1993.
PF 07-FEB-1992; 055983.
PR 07-FEB-1992; JP-055983.
PA (TOKE) TOSHIBA KK.
DR WPI; 93-308342/39.
PT Monoclonal antibody against the proteins distributed in the brain
PT - is prepd. by using rat brain extract as immunogen belonging to
PT IgG1 class which combines to rat brain extract antigen
PS Claim 2; Page 2-3; 16pp; Japanese.
CC The rat myelin sequence hybridises to the closely similar
CC sequence coding for RB35 (Q48975). The RB35 sequence was isolated
CC from a cDNA library prepared from total adult female Sprague-Dawley
CC rat brain mRNA. RB35 protein is used as an immunogen to generate
CC monoclonal antibodies of the IgG1 subtype which specifically bind
CC to a protein in rat brain extract of mol.wt. ca. 30 kD.
SQ Sequence 1164 BP; 236 A; 335 C; 327 G; 266 T;

alignment_scores:
Quality: 160.00 Length: 76
Ratio: 4.444 Gaps: 1
Percent Similarity: 47.368 Percent Identity: 46.053

alignment_block:

US-09-218-277-12 x Q48976 ..

Align seg 1/1 to: Q48976 from: 1 to: 1164

96 ThrProArgThrProProSerGlnGlyLysGlyArgGlyLeuSerLe 112
|||||
1 ACACCTCGTACACCCCTCCATCCCAAGAAAGGAGAGGCGCTGTCCT 50
112 uSerArgPheSerTrpGlyAlaGluGlyGlnArgProGlyPheGlyTyrG 129
|||||
51 CAGCAGATTTAGCTGG..... 66
129 lyGlyArgAlaSerAspTyrLysSerAlaHisLysGlyPheLysGlyVal 145
66 66
146 AspAlaGlnGlyThrLeuSerLysIlePheLysLeuGlyGlyArgAspSe 162
|||||
67GGAGGAAGACACAG 80
162 rArgSerGlySerProMetAlaArgArg 171
|||||
81 CCGCTCTGGATCTCCATAGCAAGACGC 108

seq_name: N_Geneseq_36:Q48975

seq_documentation_block:

ID Q48975 standard; cDNA to mRNA; 1147 BP.
AC Q48975;
DT 18-APR-1994 (first entry)
DE Encodes RB35 protein from rat brain.
KW RB35 antigen; immunogen; myelin; Sprague-Dawley; rat; brain;
KW antibody; IgG1; ds.
OS Rattus norvegicus (Sprague-Dawley).
PN J05219982-A.
PD 31-AUG-1993.
PF 07-FEB-1992; 055983.
PR 07-FEB-1992; JP-055983.
PA (TOKE) TOSHIBA KK.
DR WPI; 93-308342/39.
PT Monoclonal antibody against the proteins distributed in the brain
PT - is prepd. by using rat brain extract as immunogen belonging to
PT IgG1 class which combines to rat brain extract antigen
PS Claim 2; Page 2-3; 16pp; Japanese.
CC The sequence coding for RB35 was isolated from a cDNA library
CC prepared from total adult female Sprague-Dawley rat brain mRNA.

CC RB35 is used as an immunogen to generate monoclonal antibodies
 CC of the IgG1 subtype which specifically bind to a protein in rat
 CC brain extract of mol.wt. ca. 30 kD.
 SQ Sequence 1147 BP; 261 A; 331 C; 329 G; 226 T;

alignment_scores:
 Quality: 135.00 Length: 71
 Ratio: 4.355 Gaps: 1
 Percent Similarity: 43.662 Percent Identity: 43.662

alignment_block:
 US-09-218-277-12 x Q48975/rev ..

Align seg 1/1 to reverse of: Q48975 from: 1 to: 1147

101 ProProSerGlnGlyLysGlyValArgGlyLeuSerArgPheSerTrp 117
 1143 CCTCCATCCAGGAAAGGGAGGCGCTGCTCCATCAGCATTTAGCTG 1094
 117 polyAlaGluGlyGlnArgProGlyPheGlyTyrglyArgAlaSerA 134
 1093 G..... 1093
 134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyThr 150
 1093 1093
 151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerPr 167
 1092GGAGGAAGAGACACGCCCTCTGGATCTCC 1064
 167 oMetalaArgArg 171
 1063 CATGGCAAGAGCG 1051

seq_name: N_Geneseq_36:T47123

seq_documentation_block:

ID T47123 standard; CDNA; 621 BP.
 AC T47123;
 DT 11-SEP-1997 (first entry)
 DE cDNA encoding soluble fused MHC heterodimer:peptide complex pLJ13.
 KW Soluble; fusion; major histocompatibility complex; MHC;
 KW heterodimer; complex; antigen; binding groove; tolerance;
 KW autoantigen; disease; insulin dependent; diabetes mellitus; IDDM;
 KW antagonist; T cell; anergy; presenting cell; ds.
 OS Homo sapiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT mat_peptide 1..621 /*tag= a
 FT WO9640944-A2.
 PN 19-DEC-1996.
 PD 19-DEC-1996.
 PE 07-JUN-1996; U10102.
 PR 07-JUN-1995; US-482133.
 PR 07-JUN-1995; US-480002.
 PR 07-JUN-1995; US-483241.
 PR 27-OCT-1995; US-005964.
 PA (ANER-) ANERGEN INC.
 PA (ZYMO-) ZYMOGENETICS INC.
 PI Dashpande S, Gross JA, Kindsvogel W, Reich EP, Sheppard PO;
 DR WPI; 97-052337/05.
 DR P-PSDB; W10493.
 DR Novel fused major histocompatibility complex:antigenic peptide
 PT complex - useful to induce tolerance to an autoantigen-related
 PT disease e.g. insulin-dependent diabetes mellitus
 PS Example 1; Pages 118-119; 142pp; English.
 CC The present sequence encodes a novel soluble fused major
 CC histocompatibility complex (MHC) heterodimer:peptide complex,
 CC comprising 1st and 2nd MHC domains, linked by a 5-25 residue
 CC linker, and an antigenic peptide able to associate with a peptide
 CC binding groove of the MHC molecule, linked in frame to the 2nd

CC domain by a 5-25 residue linker. The complex can be used to induce
 CC immunological tolerance in adults susceptible to, or suffering from
 CC an autoantigen related disease, e.g. insulin dependent diabetes
 CC mellitus (IDDM), by antagonising the binding of particular T cells
 CC and antigen presenting cells, to induce anergy (immunological
 CC non-responsiveness) in the targeted T cell. As the heterodimers and
 CC corresponding antigen are permanently linked into a single chain,
 CC obviating the requirement for complex heterodimer truncation or
 CC formation, the complex eliminates inefficient and non-specific
 CC peptide loading.
 SQ Sequence 621 BP; 153 A; 148 C; 194 G; 126 T;

alignment_scores:

Quality: 134.00 Length: 37
 Ratio: 4.786 Gaps: 1
 Percent Similarity: 75.676 Percent Identity: 72.973

alignment_block:

US-09-218-277-12 x T47123 ..

Align seg 1/1 to: T47123 from: 1 to: 621

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99
 1 GACGAACCCAGCATGTGACATCTTTAAACATCGTGACTCGCGGTAC 50
 99 rProProSerGlnGly.....LysGlyArgGlyLeuSerLeuSerA 114
 51 ACCCCGCCCATCGGAGCGGGTCAGTGATCGGGGACACCCGACAC 100
 114 rgPheSerTrp 117
 101 GTTTCCTGTGG 111

seq_name: N_Geneseq_36:T67170

seq_documentation_block:

ID T67170 standard; DNA; 63 BP.
 AC T67170;
 DT 19-FEB-1998 (first entry)
 DE Human BPP-PE chimeric protein construction oligonucleotide Oligo 3.
 KW Pseudomonas exotoxin; myelin basic protein; chimeric protein;
 KW autoimmune disease; multiple sclerosis; human; ss.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9719179-A1.
 PD 29-MAY-1997.
 PF 17-NOV-1996; IL0151.
 PR 26-DEC-1995; IL-116559.
 PR 17-NOV-1995; IL-116044.
 PA (YISS) YISSUM RES & DEV CO.
 PI Beraud E, Lorberboun-Galski H, Marianovsky I, Steinberger I;
 PI Yarkoni S;
 DR WPI; 97-298116/27.
 PT New Pseudomonas exotoxin-myeelin basic protein chimeric proteins -
 PT used for the treatment of autoimmune diseases, particularly
 PT multiple sclerosis
 PS Claim 7; Page 22; 54pp; English.
 CC New chimeric proteins have been developed comprising a Pseudomonas
 CC aeruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)
 CC moiety selected from: (a) MBP; (b) amino acids 69-88 of guinea-pig MBP
 CC or an antigenic portion; (c) amino acids 84-102 of human MBP or an
 CC antigenic portion; (d) amino acids 143-168 of human MBP or an antigenic
 CC portion; and (e) an amino acid sequence in which one or more amino acids
 CC have been deleted, added, substituted or mutated in the amino acid
 CC sequences of (a), (b), (c), or (d), the modified sequences retaining at
 CC least 75% homology with the amino acid sequences. The present sequence
 CC represents an oligonucleotide used for constructing human BPP-PE
 CC chimeric proteins. The chimeric proteins can be used for the treatment
 CC of autoimmune diseases such as multiple sclerosis. The chimeric proteins
 CC can specifically target and kill MBP specific T cells while having no
 CC effect on non-target cells.

SQ Sequence 63 BP; 21 A; 16 C; 7 G; 19 T;

alignment_scores:
Quality: 107.00 Length: 19
Ratio: 5.632 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-218-277-12 x T67170 ..

Align seg 1/1 to: T67170 from: 1 to: 63

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99

|||||
5 GATGAATCCAGTAGTTCATTTTAAATAATATTGTAACCCACGTAC 54

99 rProPro 101

|||||

55 CCCACCC 61

seq_name: N_Geneseq_36:T67171

seq_documentation_block:

ID T67171 standard; DNA; 63 BP.

AC T67171;

DT 19-FEB-1998 (first entry)

DE Human BPP-PE chimeric protein construction oligonucleotide Oligo 5.

KW Pseudomonas exotoxin; myelin basic protein; chimeric protein;

KW autoimmune disease; multiple sclerosis; human; ss.

OS Synthetic.

PN WO9719179-A1.

PD 29-MAY-1997.

PF 17-NOV-1996; IL0151.

PR 26-DEC-1995; IL-116559.

PR 17-NOV-1995; IL-116044.

PA (YISS) YISSUM RES & DEV CO.

PI Beraud E, Lorberboun-Galski H, Marianovsky I, Steinberger I;

PI Yarkoni S;

DR WPI; 97-298116/27.

PT New Pseudomonas exotoxin-myeelin basic protein chimeric proteins -

PT used for the treatment of auto:immune diseases, particularly

PT multiple sclerosis

PS Claim 7; Page 22; 54pp; English.

CC New chimeric proteins have been developed comprising a Pseudomonas

CC aeruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)

CC moiety selected from: (a) MBP; (b) amino acids 69-88 of guinea-pig MBP

CC or an antigenic portion; (c) amino acids 84-102 of human MBP or an

CC antigenic portion; (d) amino acids 143-168 of human MBP or an antigenic

CC portion; and (e) an amino acid sequence in which one or more amino acids

CC have been deleted, added, substituted or mutated in the amino acid

CC sequences of (a), (b), (c), or (d), the modified sequences retaining at

CC least 75% homology with the amino acid sequences. The present sequence

CC represents an oligonucleotide used for constructing human BPP-PE

CC chimeric proteins. The chimeric proteins can be used for the treatment

CC of autoimmune diseases such as multiple sclerosis. The chimeric proteins

CC can specifically target and kill MBP specific T cells while having no

CC effect on non-target cells.

SQ Sequence 63 BP; 21 A; 15 C; 8 G; 19 T;

alignment_scores:

Quality: 107.00

Ratio: 5.632

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-218-277-12 x T67171 ..

Align seg 1/1 to: T67171 from: 1 to: 63

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99

|||||
5 GATGAATCCAGTAGTTCATTTTAAATAATATTGTAACCCACGTAC 54

99 rProPro 101

|||||

55 CCCACCC 61

seq_name: N_Geneseq_36:T67168

seq_documentation_block:

ID T67168 standard; DNA; 63 BP.

AC T67168;

DT 19-FEB-1998 (first entry)

DE BPP-PE chimeric protein synthesis oligonucleotide Oligo 3.

KW Pseudomonas exotoxin; myelin basic protein; chimeric protein;

KW autoimmune disease; multiple sclerosis; human; ss.

OS Synthetic.

PN WO9719179-A1.

PD 29-MAY-1997.

PF 17-NOV-1996; IL0151.

PR 26-DEC-1995; IL-116559.

PR 17-NOV-1995; IL-116044.

PA (YISS) YISSUM RES & DEV CO.

PI Beraud E, Lorberboun-Galski H, Marianovsky I, Steinberger I;

PI Yarkoni S;

DR WPI; 97-298116/27.

PT New Pseudomonas exotoxin-myeelin basic protein chimeric proteins -

PT used for the treatment of auto:immune diseases, particularly

PT multiple sclerosis

PS Claim 7; Page 9; 54pp; English.

CC New chimeric proteins have been developed comprising a Pseudomonas

CC aeruginosa exotoxin (PE) moiety linked to a myelin basic protein (MBP)

CC moiety selected from: (a) MBP; (b) amino acids 69-88 of guinea-pig MBP

CC or an antigenic portion; (c) amino acids 84-102 of human MBP or an

CC antigenic portion; (d) amino acids 143-168 of human MBP or an antigenic

CC portion; and (e) an amino acid sequence in which one or more amino acids

CC have been deleted, added, substituted or mutated in the amino acid

CC sequences of (a), (b), (c), or (d), the modified sequences retaining at

CC least 75% homology with the amino acid sequences. The present sequence

CC represents an oligonucleotide used in the synthesis of BPP-PE chimeric

CC proteins. The chimeric proteins can be used for the treatment of

CC autoimmune diseases such as multiple sclerosis. The chimeric proteins

CC can specifically target and kill MBP specific T cells while having no

CC effect on non-target cells.

SQ Sequence 63 BP; 21 A; 15 C; 8 G; 19 T;

alignment_scores:

Quality: 107.00

Ratio: 5.632

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-218-277-12 x T67168 ..

Align seg 1/1 to: T67168 from: 1 to: 63

83 AspGluAsnProValHisPhePheLysAsnIleValThrProArgTh 99

|||||

5 GATGAATCCAGTAGTTCATTTTAAATAATATTGTAACCCACGTAC 54

99 rProPro 101

|||||

55 CCCACCC 61

OM of: US-09-218-277-12 to: Issued_Patents_NA: * out_format : pfs

Date: Sep 26, 2000 8:02 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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-NORMEXT -MINLEN=0 -MAXLEN=200000000
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Search information block:

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/cgnl_7/prodata/1/lna/5C_COMB.seq:US-08-665-259-19 -		92.00	125.62	16.61	6803	1			
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/cgnl_7/prodata/1/lna/5B_COMB.seq:US-08-516-545-1 +		91.00	146.82	1.10	668	1			
/cgnl_7/prodata/1/lna/5D_COMB.seq:US-08-583-562B-7 +		91.00	121.85	26.93	8367	1			
/cgnl_7/prodata/1/lna/5D_COMB.seq:US-08-779-113-7 +		91.00	121.85	26.93	8367	1			
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/cgnl_7/prodata/1/lna/5C_COMB.seq:US-08-804-227C-7 +		90.50	104.51	248.99	44377	1			
/cgnl_7/prodata/1/lna/5D_COMB.seq:US-08-804-198-1 +		90.50	104.51	248.99	44377	1			
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/cgnl_7/prodata/1/lna/5A_COMB.seq:US-08-457-135-3 -		86.00	125.86	9.65	1556	1			
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/cgnl_7/prodata/1/lna/5C_COMB.seq:US-08-795-86B-13 +		86.00	124.08	20.25	2793	1			
/cgnl_7/prodata/1/lna/5A_COMB.seq:US-08-042-747A-7 +		86.00	123.56	21.63	2943	1			
/cgnl_7/prodata/1/lna/5C_COMB.seq:US-08-119-081-1 -		85.50	127.12	13.70	1881	1			
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/cgnl_7/prodata/1/lna/5C_COMB.seq:US-08-216-260-3 - 85.00 119.41 36.82 3762
/cgnl_7/prodata/1/lna/5A_COMB.seq:US-08-331-004A-1 - 84.50 130.85 8.49 1083
/cgnl_7/prodata/1/lna/PCPUS_COMB.seq:PCP-US95-13937A-1 - 84.50 130.85 8.49 1
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seq_documentation_block:

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; Sequence 1, Application US/08781122
; Patent No. 5948764
; GENERAL INFORMATION:
; APPLICANT: Gaur, Amitabh
; APPLICANT: Conlon, Paul J.
; TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
; TITLE OF INVENTION: UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,122
; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REFERENCE/DOCKET NUMBER: 31,392
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 622-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..513
; US-08-781-122-1
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alignment_scores:

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Quality: 922.00 Length: 171
Ratio: 5.392 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

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US-09-218-277-12 x US-08-781-122-1 ..
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1 ATGGCGTACAGAGACCTCCAGAGCGAGATCCAGTCTGGC 50
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17 aThAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArghlA 34
|||||
51 CACAGCAAGTACATGACATGCGACAGGATCGCTCTCCAGGACACA 100
|||||
34 rGaApThrGlyTleLeuAspSerIleGlyArgPhePheGlyAspArg 50
|||||
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100%
pos. 1
2

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101 GAGACAGGGGATCCTTGACTCATCGGGGCTCTTTGGGGTGACAG 150
51 GYALAPROLysArgLysSerGlyLysAspSerHisHisProAlaArg 67
151 GGTGGCCCAAGCGGGCTCTGGCAAGACTCACACCCGCGCAAGAAC 200
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAsp 84
201 TGCTCACTATGGCTCCCTGCCCCAGAGTACACGGCGGACCCCAAGATG 250
84 LuAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
251 AAAACCCCGATGCTCACTTCTTCAAGACATTTGTGACGCTCCGACACCA 300
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
301 CCCCCGTCGAGGAAAGGAGGAGGAGCTGCTCCCTGAGCAGATTAGCTG 350
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSer 134
351 GGGGGCCGAAGGCCAGAGACAGATTGGCTACGGAGCGAGCGCTCCG 400
134 sPTyrlYsSerAlaHisLysGlyPheLysGlyValAlaSpAlaGlnGlyThr 150
401 ACTATAATGGCTCACAAGGAGATTCAAGGAGATCGATGCCCGGCGACG 450
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerP 167
451 CTTTCCAAATTTTAAAGCTGGAGAGAAAGATAGTCGCTCTGATCACC 500
167 oMetAlaArgArg 171
501 CATGGCTAGACGC 513
seq_name: /gn1_7/ptodata/1/lna/PCRTUS_COMB.seq: PCT-US96-05611A-4
seq_documentation_block:
Sequence 4, Application PC/TUS9605611A
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Leonardo, Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Mettis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Sguinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995

```

```

ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: Human 18.5 kDa form of MBP
HYPOTHETICAL: No
ANTI-SENSE: No
PCT-US96-05611A-4

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alignment_scores:
Quality: 922.00 Length: 171
Ratio: 5.392 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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alignment_block:

US-09-218-277-12 x PCT-US96-05611A-4

Align seg 1/1 to: PCT-US96-05611A-4 from: 1 to: 519

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17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
54 CACAGCAATACCATGACCATGACCATGCCAGCATGGCTTCTCCCAAGGACA 103
104 GAGACAGGGGATCCTTGACTCATCGGGGCTCTTTGGCGGTGACAG 153
51 GYALAPROLysArgLysSerGlyLysAspSerHisHisProAlaArg 67
154 GGTGGCCCAAGCGGGCTCTGGCAAGACTCACACCCGCGCAAGAAC 203
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAsp 84
204 TGCTCACTATGGCTCCCTGCCCCAGAGTACACGGCGGACCCCAAGATG 253
84 LuAsnProValValHisPhePheLysAsnIleValThrProArgThrPro 100
254 AAAACCCCGATGCTCACTTCTTCAAGACATTTGTGACGCTCCGACACCA 303
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117
304 CCCCCGTCGAGGAAAGGAGGAGGAGCTGCTCCCTGAGCAGATTAGCTG 353
117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSer 134
354 GGGGGCCGAAGGCCAGAGACAGATTGGCTACGGAGCGACAGGCTCCG 403
134 sPTyrlYsSerAlaHisLysGlyPheLysGlyValAlaSpAlaGlnGlyThr 150
404 ACTATAATGGCTCACAAGGAGATTCAAGGAGTGTGATGCCCGGCGACG 453
151 LeuSerLysIlePheLysLeuGlyGlyArgAspSerArgSerGlySerP 167
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seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq: PCT-US96-05611A-1
seq_documentation_block:
: Sequence 1, Application PC/TUS9605611A
: GENERAL INFORMATION:
: APPLICANT: Mueller, John P.
: APPLICANT: Leonardo, Michael J.
: APPLICANT: McFarland, Henry F.
: APPLICANT: Matis, Louis A.
: APPLICANT: Mueller, Eileen Elliott
: APPLICANT: Nye, Steven H.
: APPLICANT: Pelfrey, Clara M.
: APPLICANT: Squinto, Stephen P.
: APPLICANT: Wilkins, James A.
: TITLE OF INVENTION: Modified Myelin Protein Molecules
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESS: Maurice M. Klee
: STREET: 1951 Burr Street
: CITY: Fairfield
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06430
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
: COMPUTER: Macintosh Centris 610
: OPERATING SYSTEM: System 7
: SOFTWARE: Microsoft Word 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/05611A
: FILING DATE: 02-MAY-1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/431,644
: FILING DATE: May 2, 1995
: APPLICATION NUMBER: 08/431,648
: FILING DATE: May 2, 1995
: APPLICATION NUMBER: 08/482,114
: FILING DATE: June 7, 1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Klee, Maurice M.
: REGISTRATION NUMBER: 30,399
: REFERENCE/DOCKET NUMBER: ALX-129
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203) 254 1400
: TELEFAX: (203) 254 1101
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 594 base pairs
: TYPE: Nucleic acid
: STRANDEDNESS: Double
: TOPOLOGY: Linear
: MOLECULE TYPE: cDNA to mRNA
: DESCRIPTION: MBP-X2Cys81/num. (Human 21.5 kD form
: DESCRIPTION: of MBP)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: PUBLICATION INFORMATION:
: AUTHORS: Roth, H. J.
: AUTHORS: Kronquist, K. E.
: AUTHORS: Kerlero de Rosbo, N.
: AUTHORS: Crandall, B. F.
: AUTHORS: Campagnoni, A. T.
: TITLE: Evidence for the Expression of Four
: TITLE: Myelin Basic Protein Variants in the
: TITLE: Developing Human Spinal Cord Through
: TITLE: cDNA Cloning
: JOURNAL: Journal of Neuroscience Research
: VOLUME: 17
: PAGES: 312 - 328
: DATE: 1987
: PCT-US96-05611A-1

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: Quality: 899.00 Length: 197
: Ratio: 5.257 Gaps: 1
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Align seg 1/1 to: PCT-US96-05611A-1 from: 1 to: 594
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51 GlyAlaProLysArgGlySerGly..... 58
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151 GGTGGCCCCAAGCGGGGCTGTGGCAAGTACCTGGCTMAAGCGGGCGG 200
58 ..... 58
201 GAGCCCTGTGCCCTCATGCCGCGACCGACGCGCTGGCTGTCAACATG 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
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251 ACAAGAGCTCACACCAACCGGCAAGACGCTCATATGCTCCCTGCC 300
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePhe 91
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301 CAGAACTCACAGCGCGCGACCAAGATGAACCCCGTAGTCCACTTC 350
91 eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGly 108
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351 CAGAAACATGTGACGCTCGCACACCAACCCCGTGGCGGGAAGGGGA 400
108 rGlyLeuSerLeuSerArgPheSerTrpGlyAlaGlnGlyLysArgPro 124
|||||
401 GAGGACTGTCCTGAGCAGATTAGCTGGGGGGCCGAAAGCCAGAGACCA 450
125 GlyPheGlyTyrGlyLysArgHisAspTyrLysSerAlaHisLysGly 141
|||||
451 GGATTGGCTACGAGGAGCAGACGCTCCGACTAATATGGCTGCACAAAG 500
141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
|||||
501 ATTCAGAGGAGTCGATGCCAGGCGACGCTTCCAAAATTTCAGCTGG 550
158 IyGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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551 GAGAAAGATAGTGCCTGTGATCACCCATGGCTAGAGCGC 591

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seq_documentation_block:
: Sequence 2, Application PC/TUS9605611A
: GENERAL INFORMATION:
: APPLICANT: Mueller, John P.
: APPLICANT: Leonardo, Michael J.
: APPLICANT: McFarland, Henry F.
: APPLICANT: Matis, Louis A.
: APPLICANT: Mueller, Eileen Elliott
: APPLICANT: Nye, Steven H.
: APPLICANT: Pelfrey, Clara M.
: APPLICANT: Squinto, Stephen P.

```

```

APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 MB storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: MBP+X2Cys81/Dact.
HYPOHETICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-2

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Alignment_scores:
Quality: 899.00      Length: 197
Ratio: 5.257        Gaps: 1
Percent Similarity: 86.802      Percent Identity: 86.802

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Alignment_block:
US-09-218-277-12 x PCT-US96-05611A-2

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Align seg 1/1 to: PCT-US96-05611A-2 from: 1 to: 612

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1 ATGGCGTCTCAGAAACGTCGTCACGCGTCACGCGCTCAATACCTGGC 50
17 aThAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51 CACGCGCCAGCACATGACCATGCGCGTCATGCGCTCTCCGCGGTCACC 100
34 rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyLysArg 50
|||||
101 GTGACACCGGATCTCTGACTTCATCGCGCTCTTGGGCGTGACCGT 150
51 GlyAlaProLysArgLysGlySerGly..... 58
|||||
151 GGTGCGCGGAACGTCGCTCTGCGCAACTGCGCGGTGTAACCGGCGG 200
58 ..... 58

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201 TAGCCCGCTGCGCTCTCATGCGCCGTACCGACCGCGCTGTGCAACATGT 250
59 .LysAspSerHisAlaProAlaArgThrAlaHisTyrGlySerLeuPro 74
|||||
251 ACAAGACTCCACCGCCGTACCGCGCTGTACCGCGCACTATGCTCTCCGCG 300
75 GlnLysSerHisGlyArgThrGlnAspGluAsnProValHisPhePh 91
|||||
301 CAGAAATCCACCGCGCTACCGACGATGAACCCGCTGGGACCTCTCT 350
91 eLysAsnIleValThrProArgThrProProSerGlnGlyLysGlyA 108
351 CAAAACATTGTGACCCCGCGGTACCGCGCGCTCTCAGGCGCAAGGCC 400
108 rGgLYLeuSerLeuSerArgPheSerTrpGlyAlaGluGlyLysArgPro 124
|||||
401 GTGCGCTGTCCCTGACCGCTTTCAGCTGGGGCGCGCAAGCGCAGCTCG 450
125 GlyPheGlyTyrGlyArgAlaSerAspLysSerAlaHisLysG1 141
|||||
451 GGCTTCGTTACGGCGCGCGCGCTCGACTATTAATCTGCTCACAAGG 500
141 yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
|||||
501 CTCMAAGCGGTGGATGCCAGGCTACCTTCTCCAAAATTTCAAACTGG 550
158 yGlyArgAspSerArgSerGlySerProMetAlaArgArg 171
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551 GCGGCGGTGATAGCGCTTGTGGCTCTCGATGGCTAACGCT 591
seq_name: /cgn1_7/plodata/1/lna/PCTUS_COMB.seq: PCT-US96-05611A-3
seq documentation block:
Sequence 3: Application PC/TUS9605611A
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Leonardo, Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Mattis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 MB storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399

```

```

REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: MBP-X2Ser81/bact.
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-3

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alignment_scores:
Quality: 899.00      Length: 197
Ratio: 5.257         Gaps: 1
Percent Similarity: 86.802      Percent Identity: 86.802

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alignment_block:
US-09-218-277-12 x PCT-US96-05611A-3 ..

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Align seg 1/1 to: PCT-US96-05611A-3 from: 1 to: 612

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1 MetalaserGlnLysArgProSerGlnArgHISglYserLysTyrLeuAl 17
1 ATGGCGTCTCAGAAAGCTCCGTCACGCTCAGCGCTCCCAAAACCTGGC 50
17 aThraLaserThrMetAspHisAlaArgHISglYpHeuProArgHISa 34
51 CACCGCCACACCATGACCATGCCGCTCATGCGCTCTGCGCGCTCACCC 100
34 rGAspThrLylleLeuAspSerLleGlyArgPheGlyArgParg 50
101 GTGACACCGGCATCTGACCTCATGCGCTTCTTTCGGCGGTGACCGT 150
51 GtYAlAPrOLysArgglYserglY..... 58
151 GGTGCCCGCAAGAGTGTCTGTGCAAAAGTCCGTGGCTGAACCGGGCCG 200
58 ..... 58
201 TAGCCCGCTGCGCTCATGACCGCTAGCCAGCGCGGCTGTGCAACATG 250
59 ..LysAspSerHISHisProAlaArgThraLisTyrGlySerLeuPro 74
251 ACAAAAGACTCCACACCGCGCTCGTACGCGGCTATGCTCCCTGCGCG 300
75 GlnLysSerHISglYArgThrglnAspGluAsnProValYAlHisPheP 91
301 CAGAAATCCACGCGCGCTGACCCAGGATGAAGAACCCGCTGTCACCTT 350
91 eLysAsnIleValThrProArgThrProProSerGlnLysglYAla 108
351 CAAAACATGTGACCCCGGCTGACCCGCGCGCTCTCAGGCGAAAGGCC 400
108 rglYLeuSerLeuSerArgPheSerTrglYAlaGluGlyGlnArgPro 124
401 GTGGCTGTGCTCGAGCCGCTTACGTGGGGCGCCGAAAGGCCGCTCCG 450
125 GlyPheGlyTyrGlyGlyArgAlaSerAspTyrLysSerAlaHisLysG 141
451 GGCTTGGCTTACGGCGCGCTGCGCTCGCATATAATCTCTCACAAGG 500
141 yPheLysGlyValAlaSPalagInLylThrLeuSerLysIlePheLys 158
501 CTTCAAAGGGGTGATGACCGAGGGTACTGTCCAAATTTTCAAACTGG 550
158 LylYlArgAspSerArgSerGlySerProMetLalArgArg 171

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551 GCGGCCGATAGCCGCTTGTGCTCTCCGATGCTAGACGT 591

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seq_name: /cgn1_7/ptodata/1/1na/PCTUS_COMB.seq:PCT-US96-05611A-26

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seq_documentation_block:

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Sequence 26, Application PC/TUS9605611A

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GENERAL INFORMATION:

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APPLICANT: Mueller, John P.

```

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APPLICANT: Leonardo, Michael J.

```

```

APPLICANT: McFarland, Henry F.

```

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APPLICANT: Matis, Louis A.

```

```

APPLICANT: Mueller, Eileen Elliott

```

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APPLICANT: Nye, Steven H.

```

```

APPLICANT: Pellety, Clara M.

```

```

APPLICANT: Squinto, Stephen P.

```

```

TITLE OF INVENTION: Modified Myelin Protein Molecules

```

```

NUMBER OF SEQUENCES: 29

```

```

CORRESPONDENCE ADDRESS:

```

```

ADDRESSEE: Maurice M. Klee

```

```

STREET: 1951 Burr Street

```

```

CITY: Fairfield

```

```

STATE: Connecticut

```

```

COUNTRY: USA

```

```

ZIP: 06430

```

```

COMPUTER READABLE FORM:

```

```

MEDIUM TYPE: 3.5 inch, 0.8 Mb storage

```

```

COMPUTER: Macintosh Centris 610

```

```

OPERATING SYSTEM: System 7

```

```

SOFTWARE: Microsoft Word 6.0.1

```

```

CURRENT APPLICATION DATA:

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```

APPLICATION NUMBER: PCT/US96/05611A

```

```

FILING DATE: 02-MAY-1995

```

```

CLASSIFICATION:

```

```

PRIOR APPLICATION DATA:

```

```

APPLICATION NUMBER: 08/431,644

```

```

FILING DATE: May 2, 1995

```

```

APPLICATION NUMBER: 08/431,648

```

```

FILING DATE: May 2, 1995

```

```

APPLICATION NUMBER: 08/482,114

```

```

FILING DATE: June 7, 1995

```

```

ATTORNEY/AGENT INFORMATION:

```

```

NAME: Klee, Maurice M.

```

```

REGISTRATION NUMBER: 30,399

```

```

REFERENCE/DOCKET NUMBER: ALX-129

```

```

TELECOMMUNICATION INFORMATION:

```

```

TELEPHONE: (203) 255 1400

```

```

TELEFAX: (203) 254 1101

```

```

INFORMATION FOR SEQ ID NO: 26:

```

```

SEQUENCE CHARACTERISTICS:

```

```

LENGTH: 1122 base pairs

```

```

TYPE: Nucleic acid

```

```

STRANDEDNESS: Double

```

```

TOPOLOGY: Linear

```

```

MOLECULE TYPE: Other nucleic acid

```

```

DESCRIPTION: MP4 chimera

```

```

HYPOTHETICAL: NO

```

```

ANTI-SENSE: NO

```

```

PCT-US96-05611A-26

```

```

alignment_scores:

```

```
Quality: 899.00      Length: 197

```

```
Ratio: 5.257         Gaps: 1

```

```
Percent Similarity: 86.802      Percent Identity: 86.802

```

```

alignment_block:

```

```
US-09-218-277-12 x PCT-US96-05611A-26 ..

```

```

Align seg 1/1 to: PCT-US96-05611A-26 from: 1 to: 1122

```

```

1 MetalaserGlnLysArgProSerGlnArgHISglYserLysTyrLeuAl 17

```

```

1 ATGGCGTCTCGAAGACGTCCCTCCAGCGTACGGCTCCAAATACCTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
51 CACCGCCAGCAGCATGGACATGCCCGCATGGCTTCTCTGCCGCGTACC 100
34 rGaAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
101 GTGACACCGCGCATCTGGACTCCATCGCGCTTCTTGGGGGTGACCGT 150
51 GAlaAlaProLysArgGlySerGly..... 58
151 GGTCCGCCGAAGACGTGGCTCTGGCAAGTGGCGGTGGCTGAACCGGGCG 200
58 ..... 58
201 TAGCCCGCTGCGGTCTCATGCCCGTAGCCAGCGGGCGCTGTGAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGAGCTCCACACCGCGCTGTACCGCGCACTATGGCTCCCTGCCG 300
75 GlnLysSerHisGlyArgThrGlnAspGlnAsnProValValHisPhePh 91
301 CAGAAATCCACGCGCGCTGACCCAGATGAAAACCGGTGGTGCACCTTCT 350
91 eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGlyA 108
351 CAAAACATTGTGACCCCGCGTACCGCGCGCGCTCAGGGCAAGGCC 400
108 rGlyLysSerLeuSerArgPheSerTrpGlyAlaGlnGlyGlnArgPro 124
401 GTGGCTGTCTCCCTAGCGGTTTCAGCTGGGGCGCGGAAGGCGACGCTCG 450
125 GAlaPheGlyTyrGlyArgAlaSerAspTyrLysSerAlaHisLysGly 141
451 GCGTTCGGTTACGGCGCGCGTGGCTCCGACTATTAATGTGCTCACAAAGG 500
141 yPheLysGlyValAlaAspAlaGlnGlyThrLeuSerLysIlePheLysLeu 158
501 CTCGAAGCGCTGATGCCCGGAGGATCTGTCCAAATTTTCAACACGG 550
158 lYgIAlaAspSerArgSerGlySerProMetAlaArg 171
551 GCGGCCGTGATAGCGGCTGTCTCGATCGGTAGACGT 591
seq_name: /cgnl_7/prodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-25
seq_documentation_block:
; Sequence 25, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 MB storage
; COMPUTER: Macintosh Centris 610
; OPERATING SYSTEM: System 7

```

```

SOFTWARE: Microsoft Word 6.0.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05611A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,644
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/431,648
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/482,114
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1155 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: MP3 chimera
; HYPOTHEICAL: No
; ANTI-SENSE: No
;
; PCT-US96-05611A-25

```

alignment_scores:

```

Quality: 899.00 Length: 197
Ratio: 5.257 Gaps: 1
Percent Similarity: 86.802 Percent Identity: 86.802

```

alignment_block:

```

US-09-218-277-12 x PCT-US96-05611A-25 ..

```

```

Align seg 1/1 to: PCT-US96-05611A-25 from: 1 to: 1155

```

```

1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
1 ATGGCGTCTCGAAGACGTCCCTCCAGCGTACGGCTCCAAATACCTGGC 50
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
51 CACCGCCAGCAGCATGGACATGCCCGCATGGCTTCTCTGCCGCGTACC 100
34 rGaAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyGlyAspArg 50
101 GTGACACCGCGCATCTGGACTCCATCGCGCGCTTCTTGGGGGTGACCGT 150
51 GAlaAlaProLysArgGlySerGly..... 58
|||||
151 GGTCCGCCGAAGACGTGGCTCTGGCAAGTGGCGGTGGAACCGGGCGG 200
58 ..... 58
201 TAGCCCGCTGCGGTCTCATGCCCGTAGCCAGCGGGCGCTGTGAACATGT 250
59 ..LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuPro 74
251 ACAAGAGCTCCACACCGCGCTGTACCGCGCACTATGGCTCCCTGCCG 300
75 GlnLysSerHisGlyArgThrGlnAspGlnAsnProValValHisPhePh 91
|||||
301 CAGAAATCCACGCGCGCTGACCCAGATGAAAACCGGTGGTGCACCTTCT 350
91 eLysAsnIleValThrProArgThrProProProSerGlnGlyLysGlyA 108
|||||
351 CAAAACATTGTGACCCCGCGTACCGCGCGCGCTCAGGGCAAGGCC 400

```

```

108  rgglyleuSerleuSerArpPheSerTrpGlyAlaGluGlyAlaArgPro 124
      |||
401  GTGGGCTCTCCCTGAGCCGTTTCAGCTGGGGCGGAGGCGCGCTCCG 450
125  glyPheGlyTYrGlyGlyArGAlaSerAspTYrLysSerAlaHisLysG1 141
      |||
451  GGCTTCGGTTACGGCGCGGCGTCCGACTATTAATCTGCTCACAAGG 500
141  yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
      |||
501  CTTCAAGAGCGGTGATGCCAGGGAACCTTGCCAAATTTTCAACACG 550
158  lyGlyArGAspSerArGSerGlySerProMetAlaArgArg 171
      |||
551  GCGGCGGTGATAGCCGTTCTGCTCTCCGATGCGTAGACGT 591

seq_name: /cgnl_7/prodata/1/lna/PCTUS_COMB.seq:PCR-US96-05611A-28

seq_documentation_block:
; Sequence 28, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Sculinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 MB storage
; COMPUTER: Macintosh Centris 610
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05611A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,644
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/431,648
; FILING DATE: May 2, 1995
; APPLICATION NUMBER: 08/482,114
; FILING DATE: June 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: ALX-129
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1476 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: MMOGp4 chimera
; HYPOTHEICAL: NO
; ANTI-SENSE: NO

```

```

PCT-US96-05611A-28

alignment_scores:
      Quality: 899.00      Length: 197
      Ratio: 5.257
      Percent Similarity: 86.802      Percent Identity: 86.802

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-28 ..
Align seg 1/1 to: PCT-US96-05611A-28 from: 1 to: 1476

1  MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTYrLeuAl 17
1  ATGGGGGTCTCAGAAACGTCCTCCACAGGCTCAGCGCTCAATACCTGGC 50
17  aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
51  CACGCGCACACATGACATGCCCGCATGGCTTCTCGCGGCTCACCC 100
34  rGAspThrGlyIleLeuAspSerIleGlyArgPhePheGlyLysArg 50
101  GTGACACCGCGCATCTGTGACTTCATCGCGCTTCTTGCGGCTGACCG 150
51  G1AlaProLysArgGlySerGly..... 58
151  GGTGGCGCGGAACGTGGCTGTGGCAAGTGGCGGTGGTGAACCGGGCG 200
58  ..... 58
201  TAGCCCGCTGCGTCTCATGCCGTAGCCAGCCGGCGCTGTCAACATGT 250
59  .LysAspSerHisProAlaArgThrAlaHisTYrGlySerLeuPro 74
251  ACAAGAGCTCCACACCCCGCTGTGACCGCACATATAGCTCCCTGGCG 300
75  GlnLysSerHisGlyArgThrGlnAspGlnAsnProValAlaHisPheP 91
301  CAGAAATCCACAGCGCGCTACCCAGATGAACCGGCTGTGCACTTCTT 350
91  eLysAsnIleValThrProArgThrProProSerGlnLysGlyA 108
351  CAAAACATTTGTGACCCCGCTACCCCGCGCTCTCAGGCAAGGCC 400
108  rgglyleuSerleuSerArpPheSerTrpGlyAlaGluGlyAlaArgPro 124
401  GTGGCTGTCCCTGAGCCGTTTCAGCTGGGGCGGAGGCGCACGCTCCG 450
125  glyPheGlyTYrGlyGlyArGAlaSerAspTYrLysSerAlaHisLysG1 141
451  GGCTTCGGTTACGGCGCGGCGTCCGACTATTAATCTGCTCACAAGG 500
141  yPheLysGlyValAspAlaGlnGlyThrLeuSerLysIlePheLysLeuG 158
501  CTTCAAGAGCGGTGATGCCAGGGAACCTTGCCAAATTTTCAACACG 550
158  lyGlyArGAspSerArGSerGlySerProMetAlaArgArg 171
551  GCGGCGGTGATAGCCGTTCTGCTCTCCGATGCGTAGACGT 591

seq_name: /cgnl_7/prodata/1/lna/PCTUS_COMB.seq:PCR-US96-05611A-27

seq_documentation_block:
; Sequence 27, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.

```

APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PM4 chimera
HYPOTHEICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-27
alignment_scores:
Quality: 894.00 Length: 196
Ratio: 5.259 Gaps: 1
Percent Similarity: 86.735 Percent Identity: 86.735
alignment_block:
US-09-218-277-12 x PCT-US96-05611A-27 ..
Align seq 1/1 to: PCT-US96-05611A-27 from: 1 to: 1125
2 AlSeGlnIySaRgProSeGlnAaGhIsGlySeRlySTyRleuAaTh 18
|||||
520 GCCTCTAGAAAGTCCTGCCAGCGCACGGCTCCAAATACCTGGCCAC 569
18 fAlaSerThMeTasPhIsAlaRgHIsGlyPhLeuPrOArGHIsArGa 35
570 CGCAGACCATGACCATGCCGTCTGCTTCCTGCGCGCTCACCGTG 619
35 sPhRcGlyIleuAaSPeRleGlyArPhpHeGlyGlyAaPaRgGly 51
|||||
620 ACACCGGCACTCGACTCCATCGCGCTTCTTCGCGGTGACCGTGT 669
52 AlAProLySaRgIySeRgLy..... 58
670 GCCCGCAAGCGTCTGCGCAAGTCCGTGGGTGAACCGGCGCTAG 719

59L 59
720 CCCGTCGCGTCTCATGCCGTAGCCAGCGGGCGCTGTCAACATGTACA 769
59 ySaSPeRlHIsPrOAlArGThRAlAHIsTyRIsGlySeRleuPrOgIn 75
|||||
770 AAGACTCCACACCGCGGCTCGACCGGCATATGCTCCCTCGCGCAG 819
76 LySeSerHIsGlyArGThRgInaSPeGluAaPrOvaIvaIHIsPhpHeLy 92
|||||
820 AATCCACGCGCGGTACCCAGATGAACCCGGTGTGCTACATTTCAA 869
92 sAaNIleValThPrOArGThRPrOPrOSeRgInGlyLySgIyArG 109
|||||
870 AAACATGTGACCCCGCGTACCCCGCGGCTCTCAGGGCAAGGCGG 919
109 LySeSerleuSeArGpHeSeRTrpGlyAlaGluGlyInArGProGly 125
|||||
920 GCCTGTCCTGAGCCCTTTCAGCTGGGGCGCGGAAGGCCAGCGTCC 969
126 PhEgLyTyRgLyGlyArGaIaSeArPyTyRlySeRAlAHIsLySgLyPh 142
|||||
970 TTGGCTACGGCGCGCGCTGCGTCCGACTATAATCTGTCAAAAGGCT 1019
142 eLySgLyVaIaSPAlaGInGlyThRleuSeRlyStIePhelySleuGly 159
|||||
1020 CAAAGCGGTGGATGCCAGGCGACCTGTCCAAATTTTCAAACTGGCG 1069
159 LyArGaSPeRArGSeRgLySeRPrOmeTAlaArGArG 171
|||||
1070 GCCGTATAGCCGTTGCTGCTCTCCGATGCTAGACGT 1107
seq.name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-8
seq.documentation_block:
Sequence 8, Application PC/TUS9605611A
GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Leonardo, Michael J.
APPLICANT: McFarland, Henry F.
APPLICANT: Matlis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelirey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.


```
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 4
HYPOTHETICAL: No
ANTI-SENSE: Yes
PCT-US96-05611A-8

alignment_scores:
Quality: 236.00      Length: 43
Ratio: 5.488         Gaps: 0
Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-8/rev ..

Align seg 1/1 to reverse of: PCT-US96-05611A-8 from: 1 to: 131

77 SerHISGLYARThrglnAspGluAsnProValValHisPhePheLysAs 93
|||||
130 TCCGAGGCGCGTACCCAGATGAAGCCGCGTGTGACATCTTCAAAAA 81
93 nileValThProArGThrProProSerGlnGlyLysGlyArgGlyL 110
|||||
80 CATTGACACCCCGCTACCCCGCGCTCTCAGGCGCAAGCGCGTGGCC 31
110 euseSerArGpHeserTrrGlyAla 119
|||||
30 TGTCCCTGAGCCGCTTTCAGCTGGGCGCC 2

seq_name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-9
seq_documentation_block:
; Sequence 9, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
; COMPUTER: Macintosh Centris 610
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05611A
; FILING DATE: 02-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 5
HYPOTHETICAL: No
ANTI-SENSE: No
PCT-US96-05611A-9

alignment_scores:
Quality: 214.00      Length: 39
Ratio: 5.487         Gaps: 0
Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-9 ..

Align seg 1/1 to: PCT-US96-05611A-9 from: 1 to: 119

114 ArgPheSerTrrGlyAlaGlnGlyGlnArgProGlyPheGlyTrrGly 130
|||||
3 CGTTTACGCTGGGGCGCGCAAGGCCAGCGTCCGGGCTTGGCTACGGCGG 52
130 yArgAlaSerAspTrrLysSerAlaHisLysGlyPheLysGlyValAsp 147
|||||
53 CCGTGGCTCCGACTATTAATCTGTCACAAAGGCTTCAAGCGGTGAGT 102
147 lagInGlyThrLysSer 152
|||||
103 CCCAGGCGACACCTGTCC 119

seq_name: /cgn1_7/ptodata/1/lna/PCTUS_COMB.seq:PCT-US96-05611A-5
seq_documentation_block:
; Sequence 5, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Wilkins, James A.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
```

```
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 1
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-5
```

```
alignment_scores:
Quality: 188.00      Length: 35
Ratio: 5.371         Gaps: 0
Percent Similarity: 100.000    Percent Identity: 100.000
```

```
alignment_block:
US-09-218-277-12 x PCT-US96-05611A-5 ..
```

```
Align seg 1/1 to: PCT-US96-05611A-5 from: 1 to: 130
```

```
1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
26 ATGGCGTCTCAGAAACGTCCTCCAGCGTCACGGCTCCAAATACCTGCG 75
|||||
17 aThrLaserThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
76 CACCGCCGACACCATGACATGCGCGTCTGCTTCTGCGCGCTCACG 125
|||||
34 rGAsp 35
|||||
126 GTGAC 130
```

```
seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-6
seq_documentation_block:
; Sequence 6, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
; TITLE OF INVENTION: Modified Myelin Protein Molecules
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
```

```
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 6:
```

```
SEQUENCE CHARACTERISTICS:
LENGTH: 129 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 2
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-05611A-6
```

```
alignment_scores:
Quality: 162.00      Length: 30
Ratio: 5.400         Gaps: 0
Percent Similarity: 100.000    Percent Identity: 100.000
```

```
alignment_block:
US-09-218-277-12 x PCT-US96-05611A-6/rev ..
```

```
Align seg 1/1 to reverse of: PCT-US96-05611A-6 from: 1 to: 129
```

```
30 LeuProArgHisArgAspThrGlyIleLeuAspSerIleGlyArgPhePh 46
|||||
128 CTGCCGCGTCAACCGTCGACACCGGCATCTGACTCCATCGCGCTTCTT 79
|||||
46 eGlyGlyAspArgGlyAlaProLysArgGlySerGlyLys 59
|||||
78 CGCGCGTGTACCGTGTGCGCGCAACGTGGCTGTGGCAA 39
```

```
seq_name: /cgn1_7/ptodata/1/ina/PCTUS_COMB.seq:PCT-US96-05611A-7
seq_documentation_block:
; Sequence 7, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matlis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
; APPLICANT: Nye, Steven H.
; APPLICANT: Pelfrey, Clara M.
; APPLICANT: Squinto, Stephen P.
```

```
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 3
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-05611A-7

alignment_scores:
Quality: 135.00 Length: 24
Ratio: 5.625 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-7 ..
Align seg 1/1 to: PCT-US96-05611A-7 from: 1 to: 133

59 LysAspSerHisHisProAlaArgThrAlaHisTyrGlySerLeuProG1 75
|||||
61 AAGAGCTCCACACCGCGGCTCGTACCGGCACATATGCTCCTGCCGCA 110
|||||
75 nlySerHisGlyArgThrGln 82
|||||
111 GAATCCACGAGCGCGTACCCAG 132

seq_name: /sgnl7/ptodata/1/lna/PCTUS.COMB.seq:PCT-US96-05611A-10
seq_documentation_block:
; Sequence 10, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Leonardo, Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
```

```
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-129
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 bases
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PCR primer oligonucleotide 6
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US96-05611A-10

alignment_scores:
Quality: 130.00 Length: 25
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-218-277-12 x PCT-US96-05611A-10/rev ..
Align seg 1/1 to reverse of: PCT-US96-05611A-10 from: 1 to: 111

146 AspAlaGlnGlyThrLeuSerLysIlePheLysLeuGlyArgAspse 162
|||||
110 GATGCCACGAGCGACCTGTCACAAATTTTCAAACTGCGCGCGTGATAG 61
|||||
162 ArgSerGlySerProMetAlaArgArg 171
|||||
60 CGGTTGCGCTTCGCGATGCTAGACGT 33
```

1
.
26

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:34:34 ; Search time 12.55 Seconds

(Without alignments)
843.211 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171

Sequence: 1 MASQKRPSSGRHSKYLATAS.....SKIFKLGDRSGSGSPMAR 171

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 178050 seqs, 61884766 residues

Word size : 0

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: PIR.64:*
2: PIR1:*
3: PIR2:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	66.1	197	1 MBHUB	myelin basic prote
2	76	44.4	171	1 MBICZB	myelin basic prote
3	46	26.9	128	1 MBRTS	myelin basic prote
4	46	26.9	167	2 A37246	myelin basic prote
5	45	26.3	328	1 MBMSB	golli-myelin basic
6	41	24.0	169	1 MBBOB	myelin basic prote
7	41	24.0	171	1 MBPGB	myelin basic prote
8	14	8.2	14	2 S12904	protein kinase (EC
9	12	7.0	42	2 B92087	myelin basic prote
10	12	7.0	174	2 S08535	myelin basic prote
11	11	6.4	33	2 A60222	myelin basic prote
12	12	6.4	88	2 T43964	myelin basic prote
13	7	4.1	88	2 T44170	hypothetical prote
14	7	4.1	93	2 T09318	u24 [imported] - h
15	7	4.1	123	2 A69884	EcoFI protein - hu
16	7	4.1	128	2 A60215	cell wall protein
17	7	4.1	155	2 B32989	myelin basic prote
18	7	4.1	155	2 T17889	myelin basic prote
19	7	4.1	259	2 T29727	glycine-rich prote
20	7	4.1	332	2 E70384	hypothetical prote
21	7	4.1	368	2 S64487	biotin synthetase
22	7	4.1	481	2 T56246	GTP-binding protei
23	7	4.1	508	1 NDBE33	lipopolysaccharide
24	7	4.1	529	2 A47131	exonuclease (EC 3.
25	7	4.1	532	2 T42593	Na+-dependent neut
26	7	4.1	532	2 T37188	neutral amino acid
27	7	4.1	545	2 T02279	neutral amino acid
28	7	4.1	565	2 T42593	hypothetical prote
29	7	4.1	573	2 S44605	exonuclease (EC 3.

ALIGNMENTS

30	7	4.1	839	2 T39190	probable ATP-depen
31	7	4.1	1151	2 T18535	high molecular mas
32	7	4.1	1345	2 T41960	major capsid prote
33	7	4.1	3305	2 T18358	apolipoprotein prec
34	6	3.5	60	2 A57413	band 3 anion trans
35	6	3.5	88	2 S38267	cuticle protein Im
36	6	3.5	96	2 G70117	conserved hypochet
37	6	3.5	102	2 S61055	probable membrane
38	6	3.5	109	2 B72213	conserved hypochet
39	6	3.5	113	2 S13494	major oleosin chat
40	6	3.5	115	2 A23925	proline-rich phosph
41	6	3.5	116	2 S39434	spermathecin AON-3
42	6	3.5	116	2 S17567	AON-3 protein - pl
43	6	3.5	124	2 S49957	hypothetical prote
44	6	3.5	125	2 S21419	hypothetical 14.4K
45	6	3.5	132	2 T21416	hypothetical prote

RESULT 1

MBHUB
myelin basic protein - human
N:Contains: myelin basic protein precursor, 17.2K splice form; myelin basic protein p
.5K splice form
C:Species: Homo sapiens (man)
C:Date: 18-Dec-1981 #sequence, revision 25-Aug-1995 #text, change 22-Jun-1999
C:Accession: S10482; A94106; B94106; A90256; JH0802; A60862; A61420; A33273; I54219;
R:Streicher, R.; Stoffel, W.
Bio. Chem. Hoppe-Seyler 370, 503-510, 1989
A:Title: The organization of the human myelin basic protein gene. Comparison with the
A:Reference number: S10482; MUID:89302693
A:Accession: S10482
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-197 <STR>
A:Cross-references: EMBL:X17286; NID:q34490; PIDN:CMA35179.1; PID:e221974; PID:g11842
R:Kamholz, J.; De Ferra, F.; Puckett, C.; Lazzarini, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 4962-4966, 1986
A:Title: Identification of three forms of human myelin basic protein by cDNA cloning.
A:Reference number: A94106; MUID:86259714
A:Accession: A94106
A:Molecule type: mRNA
A:Residues: 1-59, 86-197 <KAM>
A:Cross-references: GB:M13577; NID:q187408; PIDN:AA59562.1; PID:g307160
A:Note: 18.5K splice form
A:Accession: B94106
A:Molecule type: mRNA
A:Residues: 1-197 <KA2>
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form
A:Note: a 17.2K splice form is also described
A:Note: antibody to the exon 2 encoded sequence detected a 21.5K splice form; a 17.2K
R:Carnegie, P.R.
Biochem. J. 123, 57-67, 1971
A:Title: Amino acid sequence of the encephalitogenic basic protein from human myelin.
A:Reference number: A90256; MUID:72066400
A:Accession: A90256
A:Molecule type: protein
A:Residues: 2-59, 86-197 <CAR>
R:Proost, P.; Van Damme, J.; Opdenakker, G.
Biochem. Biophys. Res. Commun. 192, 1175-1181, 1993
A:Title: Leukocyte gelatinase B cleavage releases encephalitogens from human myelin b
A:Reference number: JH0802; MUID:93282820
A:Accession: JH0802
A:Molecule type: protein
A:Residues: 2-59, 86-197 <PRO>
A:Experimental source: Brain
R:Scoble, H.A.; Whitaker, J.N.; Biemann, K.
J. Neurochem. 47, 614-616, 1986
A:Title: Analysis of the primary sequence of human myelin basic protein peptides 1-44
A:Reference number: A60862; MUID:86280476
A:Accession: A60862

A:Molecule type: protein
 A:Residues: 2-45,117-197 <SCO>
 A:Note: evidence for acetylated amino end
 R:Gibson, B.W.; Gilliom, R.D.; Whitaker, J.N.; Blemann, K.
 J. Biol. Chem. 259, 5028-5031, 1984
 A:Title: Amino acid sequence of human myelin basic protein peptide 45-89 as determined by mass spectrometry
 A:Reference number: A61420; MID:84185608
 A:Accession: A61420
 A:Molecule type: protein
 A:Residues: 46-59,86-116 <GIB>
 R:Wood, D.D.; Moscarello, M.A.
 J. Biol. Chem. 264, 5121-5127, 1989
 A:Title: The isolation, characterization, and lipid-aggregating properties of a citrullinized myelin basic protein peptide
 A:Reference number: A33273; MID:8914797
 A:Accession: A33273
 A:Molecule type: protein
 A:Residues: 15-25, 'X', 27-31, 'X', 33-59, 86-148, 'X', 150-156, 'X', 158-185, 'X', 187-196, 'X' <MC>
 A:Note: form C-8; residues designated 'X' were determined as citrulline
 R:Baladin, G.S.; Carnegie, P.R.
 Biochem. J. 123, 69-74, 1971
 A:Title: Isolation and partial characterization of methylated arginines from the encephalic myelin basic protein
 A:Reference number: A90257; MID:72066401
 A:Accession: A90257
 A:Contents: annotation: methylarginine
 A:Note: Arg-134 may be unmodified, monomethylarginine, or dimethylarginine in the approx 100% of the protein
 R:Immon, V.A.; Wilks, A.V.; Carnegie, P.R.
 J. Immunol. 105, 1223-1230, 1971
 A:Reference number: A92806; MID:71088405
 A:Contents: annotation
 A:Note: a region including residues 139-149 induces experimental autoimmune encephalomyelitis in the rat
 R:Boylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.E.; Prinsner, S.B.
 Genomics 6, 16-22, 1990
 A:Title: Repetitive DNA (TGGA)_n 5' to the human myelin basic protein gene: a new form of myelin basic protein
 A:Reference number: D54219; MID:90152679
 A:Accession: D54219
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-59 <RES>
 A:Cross-references: GB:M63599; NID:q187402; PIDN:AA59560.1; PID:q187403
 R:Roth, H.J.; Krongauz, K.E.; Keriolo de Rosbo, N.; Crandall, B.F.; Campagnoni, A.T.
 J. Neurosci. Res. 17, 321-328, 1987
 A:Title: Evidence for the expression of four myelin basic protein variants in the developing rat brain
 A:Reference number: I56567; MID:87311781
 A:Accession: I56567
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-132,144-197 <RE2>
 A:Cross-references: GB:M30516; NID:q187410; PIDN:AA59563.1; PID:q307161
 A:Accession: I73634
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-197 <RE3>
 A:Cross-references: GB:M30515; NID:q187412; PIDN:AA59564.1; PID:q307162
 R:Roth, H.J.; Krongauz, K.; Preorius, P.J.; Crandall, B.F.; Campagnoni, A.T.
 J. Neurosci. Res. 16, 227-238, 1986
 A:Title: Isolation and characterization of a cDNA coding for a novel human 17.3k myelin basic protein
 A:Reference number: I56565; MID:86380101
 A:Accession: I56565
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-59, 86-133, 145-197 <RE4>
 A:Cross-references: GB:M30047; NID:q187400; PIDN:AA59559.1; PID:q307159
 R:Roth, H.J.; Pang, H.; Mastromarini, F.; Moscarello, M.A.
 Arch. Biochem. Biophys. 322, 174-182, 1995
 A:Title: The isolation and characterization of four myelin basic proteins from the unbound myelin basic protein fraction
 A:Reference number: S66383; MID:96004793
 A:Accession: S66383
 A:Molecule type: protein
 A:Residues: 23-25, 'X', 27-39 <BOU>
 C:Comment: Four alternatively spliced forms of myelin basic protein have been observed, C:Genetics:
 A:Gene: GDB:MBP
 A:Cross-references: GDB:119379; OMIM:159430
 A:Map position: 18q22-18qter

A:Introns: 59/3; 85/3; 120/3; 132/3; 143/3; 183/3
 C:Function:
 A:Description: probably helps maintain myelin structure
 C:Superfamily: myelin basic protein
 C:Keywords: acetylated amino end; alternative splicing; citrulline; experimental auto
 F:2-197/Product: myelin basic protein, 21.5k splice form #status predicted <MBP>
 F:2-132,144-197/Product: myelin basic protein, 20.2k splice form #status predicted <M>
 F:2-59,86-133/Product: myelin basic protein, 18.5k splice form #status experimental <F>
 F:2-59,86-132,144-197/Product: myelin basic protein, 17.2k splice form #status predicted <F>
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental
 F:26,32,149,157,186,197/Modified site: citrulline (Arg) (in form C-8) #status experimental
 F:134/Modified site: omega-N-methylarginine or omega-N-omega-N'-dimethylarginine (Arg)
 Query Match 66.1%; Score 113; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 2,36-112;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 59 KDSHNPARTAHYGSGLPQKSHGRTODENPVHFFKNIVPTPTPPSGKRGSLSRFSWG 118
 |||||||
 Db 85 KDSHNPARTAHYGSGLPQKSHGRTODENPVHFFKNIVPTPTPPSGKRGSLSRFSWG 144
 Oy 119 AEGORPFGYGGASPDYKSAHKGFGVDAGTLTKFKLGGDRSGSPMAR 171
 |||||||
 Db 145 AEGORPFGYGGASPDYKSAHKGFGVDAGTLTKFKLGGDRSGSPMAR 197
 RESULT 2
 MBP2B
 myelin basic protein - chimpanzee (tentative sequence)
 N:Alternate names: MBP
 C:Species: Pan troglodytes (chimpanzee)
 C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 06-Sep-1996
 C:Accession: A03139
 R:Westall, F.C.; Thompson, M.; Kalter, S.S.
 Life Sci. 17, 219-223, 1975
 A:Title: The proposed sequence of the encephalitogenic protein from chimpanzee brain.
 A:Reference number: A03139; MID:76009821
 A:Accession: A03139
 A:Molecule type: protein
 A:Residues: 1-171 <MES>
 C:Comment: This protein may function in maintaining the proper structure of myelin.
 C:Superfamily: myelin basic protein
 C:Keywords: blocked amino end; methylated amino acid; myelin; structural protein
 F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
 F:107/Modified site: omega-N-methylarginine or omega-N-omega-N'-dimethylarginine (Arg)
 Query Match 44.4%; Score 76; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 4,46-73;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 ASQKRPDSQHSKYLTASTMDHARGLPRHRDGIIDISIRFGGDCAPKRSKSDS 61
 |||||||
 Db 1 ASQKRPDSQHSKYLTASTMDHARGLPRHRDGIIDISIRFGGDCAPKRSKSDS 60
 Oy 62 HHPARTAHYGSGLPQK 77
 |||||||
 Db 61 HHPARTAHYGSGLPQK 76
 RESULT 3
 MBP2S
 myelin basic protein S - rat
 N:Alternate names: small myelin basic protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Apr-1984 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
 C:Accession: B24351; A90275; A94243; A21062; A03142
 R:Schich, M.; Budinski, R.M.; Stoffel, W.
 Biol. Chem. Hoppe-Seyler 367, 825-834, 1986
 A:Title: Cloned proteolipid protein and myelin basic protein cDNA. Transcription of t
 A:Reference number: A24351; MID:87026249
 A:Accession: B24351

A:Molecule type: mRNA
 A:Residues: 1-128 <SCH>
 A:Cross-references: EMBL:M25889; NID:g205321; PIDN:AAA41575.1; PID:g205322
 R:Dunkley, P.R.; Carnegie, P.R.
 Biochem. J. 141, 243-255, 1974
 A:Title: Amino acid sequence of the smaller basic protein from rat brain myelin.
 A:Reference number: A90275; MUID:75127355
 A:Accession: A90275
 A:Molecule type: protein
 A:Residues: 2-128 <DUN>
 A:Note: at position 105, arginine, monomethylarginine, and dimethylarginine occur in the
 R:McFarlin, D.E.; Blank, S.E.; Kibler, R.F.; McKneally, S.; Shapira, R.
 Science 179, 478-480, 1973
 A:Title: Experimental allergic encephalomyelitis in the rat: response to encephalitogen
 A:Reference number: A94243; MUID:73180720
 A:Accession: A94243
 A:Molecule type: protein
 A:Residues: 46-86 <MCF>
 A:Note: the sequence reported for this encephalitogenic peptide differs from that shown
 R:Roach, A.; Boylan, K.; Horvath, S.; Prusiner, S.B.; Hood, L.E.
 Cell 34, 799-806, 1983
 A:Title: Characterization of cloned cDNA representing rat myelin basic protein: absence
 A:Reference number: A21062; MUID:84026484
 A:Accession: A21062
 A:Molecule type: mRNA
 A:Residues: 1-124, 1, 126-128 <ROA>
 A:Experimental source: strain Sprague-Dawley
 C:Superfamily: myelin basic protein
 C:Keywords: alternative splicing; blocked amino end; experimental autoimmune encephalomy
 F, 2-128/Product: myelin basic protein S #status experimental <MCF>
 F, 2/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #statu
 F, 105/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg) (

Query Match 26.9%; Score 46; DB 1; Length 128;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-41;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASQKRPQSRHSGSKYLATASTMDHARRHGFLEPRHDTGILDSIGRFF 46
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MASQKRPQSRHSGSKYLATASTMDHARRHGFLEPRHDTGILDSIGRFF 46

RESULT 4
 A37246
 myelin basic protein - guinea pig
 N:Alternate names: myelin A1 protein
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 07-Oct-1994
 C:Accession: A37246; C92087; A03140
 R:Deibler, G.E.; Martenson, R.E.; Krutzsch, H.C.; Kies, M.W.
 J. Neurochem. 43, 100-105, 1984
 A:Title: Sequence of guinea pig myelin basic protein.
 A:Reference number: A37246; MUID:84215086
 A:Accession: A37246
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-167 <DEI>
 R:Shapira, R.; McKneally, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971
 A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bovin
 A:Reference number: A92087
 A:Accession: C92087
 A:Molecule type: protein
 A:Residues: 45-87 <SHA>
 C:Superfamily: myelin basic protein
 C:Keywords: myelin

Query Match 26.9%; Score 46; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 3, 4e-41;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRPQSRHSGSKYLATASTMDHARRHGFLEPRHDTGILDSIGRFF 47
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 1 ASQKRPQSRHSGSKYLATASTMDHARRHGFLEPRHDTGILDSIGRFF 46

RESULT 5
 MEMSB
 golli-myelin basic protein precursor - mouse
 N:Alternate names: golli-mbp protein; MBP
 N:Contains: myelin basic protein
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Mar-1987 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999
 C:Accession: A45421; B45421; A90875; A90867; A26591; B26591; A60920; I48407; I58996;
 R:Campagnoni, A.T.; Pribyl, T.M.; Campagnoni, C.W.; Kamp, K.; Amur-Umarjee, S.; Land
 J. Biol. Chem. 268, 4930-4938, 1993
 A:Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase gene tha
 A:Reference number: A45421; MUID:93186801
 A:Accession: A45421
 A:Molecule type: mRNA
 A:Residues: 1-190; 217-276; 316-328 <CAM1>
 A:Cross-references: GB:I07507; NID:g193584
 A:Experimental source: clone J37
 A:Accession: B45421
 A:Note: sequence extracted from NCBI backbone (NCBIN:126696) and modified
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-191, 'SSEP' <CAM2>
 A:Cross-references: GB:I07508; NID:g193586; PIDN:AAA37721.1; PID:g193587
 A:Experimental source: clone Bg21
 A:Note: sequence extracted from NCBI backbone (NCBIN:126700; NCBI:P.126715)
 R:de Ferra, F.; Engh, H.; Hudson, L.; Kamholz, J.; Puckett, C.; Molleaux, S.; Lazzar
 Cell 43, 721-727, 1985
 A:Title: Alternative splicing accounts for the four forms of myelin basic protein.
 A:Reference number: A90875; MUID:86079555
 A:Accession: A90875
 A:Molecule type: mRNA
 A:Residues: 134-328 <DEF>
 A:Cross-references: GB:M1004; GB:M1169; NID:g199060; PIDN:AAA39502.1; PID:g387419
 A:Experimental source: 21.5K
 R:Takahashi, N.; Roach, A.; Teplow, D.B.; Prusiner, S.B.; Hood, L.
 Cell 42, 139-148, 1985
 A:Title: Cloning and characterization of the myelin basic protein gene from mouse: on
 A:Reference number: A90867; MUID:85254913
 A:Accession: A90867
 A:Molecule type: DNA
 A:Residues: 134-190; 217-328 <TAK>
 A:Cross-references: GB:M11533; NID:g199044; PIDN:AAA39496.1; PID:g387414
 A:Experimental source: 18.5K
 R:Newman, S.; Kitamura, K.; Campagnoni, A.T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 886-890, 1987
 A:Title: Identification of a cDNA coding for a fifth form of myelin basic protein in
 A:Reference number: A94188; MUID:87118269
 A:Accession: A26591
 A:Molecule type: mRNA
 A:Residues: 134-274; 316-328 <NEW1>
 A:Cross-references: GB:M1560; NID:g199048; PIDN:AA859711.1; PID:g199049
 A:Experimental source: clone M722; splice form 17.2K
 A:Accession: B26591
 A:Molecule type: mRNA
 A:Residues: 134-190; 217-263; 275-328 <NEW2>
 A:Cross-references: GB:M15062; NID:g199050
 R:Kitamura, K.; Newman, S.U.; Campagnoni, C.W.; Verdi, J.M.; Mohandas, T.; Handley, V
 J. Neurochem. 54, 2032-2041, 1990
 A:Title: Expression of a novel transcript of the myelin basic protein gene.
 A:Reference number: A60920; MUID:90250449
 A:Accession: A60920
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 134-190; 217-274; 316-328 <KIT>
 A:Experimental source: M41; splice form 14K

R:Grlma, B.; Zelenika, D.; Pessac, B.
 J. Neurochem. 59, 2318-2323, 1992
 A>Title: A novel transcript overlapping the myelin basic protein gene.
 A:Reference number: 148407; MUID:93057537
 A:Accession: 148407
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-191, 'SSEP' <GR1>
 A:Cross-references: EMBL:X67319; NID:951332; PIDN:CA47733.1; PID:951333
 A>Note: submitted to the EMBL Data Library, July 1992
 R:Zeller, N.K.; Hunkeler, M.J.; Campagnoni, A.T.; Sprague, J.; Lazzerini, R.A.
 Proc. Natl. Acad. Sci. U.S.A. 81, 18-22, 1984
 A>Title: Characterization of mouse myelin basic protein messenger RNAs with a myelin bas
 A:Reference number: 158996; MUID:84119431
 A:Accession: 158996
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 219-248 <ZEL>
 A:Cross-references: GB:K00989; NID:9199037; PIDN:AAA39495.1; PID:9554195
 R:Miura, M.; Tamura, T.
 Gene 75, 31-38, 1989
 A>Title: The promoter elements of the mouse myelin basic protein gene function efficient
 A:Reference number: 154033; MUID:89252919
 A:Accession: 154033
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 134-157 <MTU>
 A:Cross-references: GB:M24410; NID:9199052; PIDN:AAA39498.1; PID:9554196
 R:Okano, H.; Tamura, T.; Miura, M.; Aoyama, A.; Ikenaka, K.; Oshimura, M.; Mikoshiba, K.
 EMBO J. 7, 77-83, 1988
 A>Title: Gene organization and transcription of duplicated MBP genes of myelin deficient
 A:Reference number: 153256; MUID:88196094
 A:Accession: 153256
 A>Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 217-229, 'NH', 232-250 <OKA>
 A:Cross-references: GB:M36275; NID:9199069; PIDN:AAA39504.1; PID:9293725
 A>Note: hypothetical translation of the reversed and complementary sequence to that show
 C:Comment: Mice have five forms of myelin basic protein: 21.5K, 18.5K, 17.2K, 17.2K and
 C:Genetics:
 A:Gene: Goll1-mbp; sh1-mld
 A:Introns: 190/3; 250/3; 262/3; 273/3; 314/3
 C:Function:
 A:Description: probably helps maintain myelin structure
 C:Superfamily: myelin basic protein
 C:Keywords: alternative splicing; myelin; structural protein
 F:1-190,217-276,316-328/Product: Goll1-mbp protein (clone J37) #status predicted <MA1>
 F:134-328/Product: myelin basic protein, splice form 21.5K #status predicted <MA1>
 F:134-274,316-328/Product: myelin basic protein, splice form 17K-a #status predicted <MA
 F:134-190,217-328/Product: myelin basic protein, splice form 18.5K #status predicted <MA
 F:134-190,217-263,275-328/Product: myelin basic protein, splice form 17K-b #status predi
 F:134-190,217-274,316-328/Product: myelin basic protein, splice form 14K #status predict

Query Match 26.3%; Score 45; DB 1; Length 328;
 Best Local Similarity 100.0%; Pred. No. 7e-40;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 HGRDQENPVVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 122
 DB 234 HGRDQENPVVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 278

RESULT 6
 MBOB
 Myelin basic protein - bovine
 N:Alternate names: myelin A1 protein
 N:Contains: myelin peptide amide-12 (MPA-12); myelin peptide amide-16 (MPA-16)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 18-Dec-1981 #sequence revision 18-Dec-1981 #text change 07-May-1999
 C:Accession: A92089; A92160; A92087; S54343; A61641; B61641; A03140
 R:Eylar, E.H.; Brostoff, S.; Hashim, G.; Caccam, J.; Burnett, P.
 J. Biol. Chem. 246, 5770-5784, 1971

A>Title: Basic A1 protein of the myelin membrane. The complete amino acid sequence.
 A:Reference number: A92089; MUID:72007306
 A:Accession: A92089
 A:Molecule type: protein
 A:Residues: 17'S', 2-169 <EYL>
 R:Brostoff, S.W.; Reuter, W.; Hichens, M.; Eylar, E.H.
 J. Biol. Chem. 249, 559-567, 1974
 A>Title: Specific cleavage of the A1 protein from myelin with cathepsin D.
 A:Reference number: A92160; MUID:74070688
 A:Accession: A92160
 A:Molecule type: protein
 A:Residues: 1-169 <BRO>
 R:Shapiro, R.; McKeally, S.S.; Chou, F.; Kibler, R.F.
 J. Biol. Chem. 246, 4630-4640, 1971
 A>Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bo
 A:Reference number: A92087
 A:Accession: A92087
 A:Molecule type: protein
 A:Residues: 43-87 <SHA>
 R:Okazaki, K.; Obara, N.H.; Inoue, S.; Hidaka, H.
 Biochem. J. 306, 551-555, 1995
 A>Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in g
 A:Reference number: S54343; MUID:95194333
 A:Accession: S54343
 A:Molecule type: protein
 A:Residues: 74-75, 'HG', 78-82, 'D', 84-88, 105, 'X', 107-108, 'X', 110-114, 'X', 116-119 <OKA>
 R:Takamatsu, K.; Tatemoto, K.
 Neurochem. Res. 17, 239-246, 1992
 A>Title: Isolation and characterization of two novel peptide amides originating from
 A:Reference number: A61641; MUID:92319189
 A:Accession: A61641
 A:Molecule type: protein
 A:Residues: 1-12 <TAK>
 A:Accession: B61641
 A:Molecule type: protein
 A:Residues: 1-16 <RA2>
 A>Note: these peptides have carboxyl-terminal amides probably produced by a non-enzym
 R:Brostoff, S.; Eylar, E.H.
 Proc. Natl. Acad. Sci. U.S.A. 68, 765-769, 1971
 A>Title: Localization of methylated arginine in the A1 protein from myelin.
 A:Reference number: A93777; MUID:71153946
 A:Accession: A93777
 A:Contents: annotation
 A>Note: Arg-106 is modified to monomethylarginine and dimethylarginine
 R:Eylar, E.H.; Caccam, J.; Jackson, J.C.; Westall, F.C.; Robinson, A.B.
 Science 168, 1220-1223, 1970
 A>Title: Experimental allergic encephalomyelitis: synthesis of disease-inducing site
 A:Reference number: A94241; MUID:70176977
 A:Contents: annotation
 A>Note: the region including residues 114-122 induces experimental allergic encephalo
 C:Superfamily: myelin basic protein
 C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune ence
 F:1-169/Product: myelin basic protein #status experimental <MA1>
 F:1-16/Product: myelin peptide amide-16 #status experimental <PA16>
 F:1-12/Product: myelin peptide amide-12 #status experimental <PA12>
 F:1/Modified site: acetylated amino end (Ala) #status experimental
 F:12/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide
 F:16/Modified site: amidated carboxyl end (Ala) (amide in mature form myelin peptide
 F:106/Modified site: omega-N-methylarginine or omega-N-omega-N'-dimethylarginine (Arg

Query Match 24.0%; Score 41; DB 1; Length 169;
 Best Local Similarity 100.0%; Pred. No. 7.2e-36;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 QDENPVVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 122
 DB 80 QDENPVVHFFKNIVPRPPPSQGRGLSLRFSWGAEQ 120

RESULT 7
 MBOB
 Myelin basic protein - pig (tentative sequence)
 N:Alternate names: myelin A1 protein

N:Contains: myelin basic protein amide 14
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Apr-1996 #sequence_revision 26-Apr-1996 #text_change 07-May-1999
C:Accession: A61640; A36245
R:Kira, J.; Delbier, G.E.; Kruttsch, H.C.; Martenson, R.E.
J. Neurochem. 44, 134-142, 1985
A:Title: Amino acid sequence of porcine myelin basic protein.
A:Reference number: A61640; MUID:85036964
A:Accession: A61640
A:Molecule type: protein
A:Residues: 1-171 <KIR>
A:Note: some peptides were ordered by homology
R:Takamatsu, K.; Tatemoto, K.
Biochem. Biophys. Res. Commun. 172, 1167-1174, 1990
A:Title: Isolation and characterization of a novel peptide amide from porcine brain.
A:Reference number: A36245; MUID:91058553
A:Accession: A36245
A:Molecule type: protein
A:Residues: 1-14 <TRK>
A:Note: the sequence in the abstract is inconsistent with that in figure 3 in having Glu
A:Note: this peptide has a carboxyl-terminal amide probably produced by a non-enzymatic
C:Superfamily: myelin basic protein
C:Keywords: acetylated amino end; amidated carboxyl end; experimental autoimmune enceph
F:1-17/Product: myelin basic protein #status experimental <MAT>
F:1-14/Product: myelin peptide amide-14 #status experimental <PAL2>
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:1/Modified site: amidated carboxyl end (Tyr) (amide in mature form myelin peptide am
F:107/Modified site: omega-N-methylarginine or omega-N'-dimethylarginine (Arg) (

Query Match 24.0%; Score 41; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.3e-36;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 82 QDENPVVHFKNIVTPRPPSGKRGSLSRFSWGAEQ 122
DB 81 QDENPVVHFKNIVTPRPPSGKRGSLSRFSWGAEQ 121

RESULT 8
S12904
Protein kinase (EC 2.7.1.37) - starfish (Plaster ochraceus)
C:Species: Plaster ochraceus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C:Accession: S12904
R:Sanjhera, J.S.; Aebersold, R.; Morrison, H.D.; Bures, E.J.; Pelech, S.L.
FEBS Lett. 273, 223-226, 1990
A:Title: Identification of the sites in myelin basic protein that are phosphorylated by
A:Reference number: S12904; MUID:91032186
A:Accession: S12904
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SAN>
C:Keywords: phosphotransferase

Query Match 8.2%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 93 NIVTPRPPPSQK 106
DB 1 NIVTPRPPPSQK 14

RESULT 9
B92087
myelin basic protein - rabbit (fragment)
N:Alternate names: myelin AI protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 30-Sep-1993
C:Accession: B92087; A03140
R:Shapira, R.; McKeenly, S.S.; Chou, F.; Kibler, R.F.

J. Biol. Chem. 246, 4630-4640, 1971
A:Title: Encephalitogenic fragment of myelin basic protein. Amino acid sequence of bo
A:Reference number: A92087
A:Accession: B92087
A:Molecule type: protein
A:Residues: 1-42 <SHR>
C:Superfamily: myelin basic protein
C:Keywords: myelin

Query Match 7.0%; Score 12; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 49 DRGAPKRGSGKD 60
DB 4 DRGAPKRGSGKD 15

RESULT 10
S08535
myelin basic protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 13-Aug-1999
C:Accession: S08535
R:Zopf, D.; Sonntag, V.; Betz, H.; Gundelfinger, E.D.
Glia 2, 241-249, 1989
A:Title: Developmental accumulation and heterogeneity of myelin basic protein transcr
A:Reference number: S08535; MUID:89358239
A:Accession: S08535
A:Molecule type: mRNA
A:Residues: 1-174 <ZOP>
A:Cross-references: EMBL:X17103; NID:963594; PIDN:CAA34959.1; PID:963595
C:Superfamily: myelin basic protein

Query Match 7.0%; Score 12; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 148 QGTLSKIFKLG 159
DB 147 QGTLSKIFKLG 158

RESULT 11
A60222
myelin basic protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 17-Jul-1994
C:Accession: A60222
R:Aruga, J.; Okano, H.; Mikoshiba, K.
J. Neurochem. 56, 1222-1226, 1991
A:Title: Identification of the new isoforms of mouse myelin basic protein: the existe
A:Reference number: A60222; MUID:91162193
A:Accession: A60222
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-33 <ARU>

Query Match 6.4%; Score 11; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 107 GRGLSRFSW 117
DB 23 GRGLSRFSW 33

RESULT 12
T43984
hypothetical protein U24 [imported] - human herpesvirus 6 (strain HST)

C:Species: human herpesvirus 6
A:Variety: strain HST
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43984
R:Issawa, Y.; Mukai, T.; Nakano, K.; Kagawa, M.; Chen, J.; Mori, Y.; Sunagawa, T.; Kawa
J. Virol. 73, 8053-8063, 1999
A:Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A:Reference number: 222732
A:Accession: T43984
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-88 <ISE>
A:Cross-references: EMBL:AB021506; PIDN:BA478245.1
A:Experimental source: strain HST; pop. variant B
C:Genetics:
A:Note: U24

Query Match 4.1%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 PRTPPS 103
|||||
DB 4 PRTPPS 10

RESULT 13
U24 [imported] - human herpesvirus 6 (strain Z29)
C:Species: human herpesvirus 6
A:Variety: strain Z29
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44170
R:Domínguez, G.; Dambaug, T.R.; Stamey, F.R.; Dewhurst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1999
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with human
A:Reference number: 222734; MUID:99412318
A:Accession: T44170
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-88 <DOM>
A:Cross-references: EMBL:AF157706; PIDN:AA049637.1
A:Experimental source: strain Z29; variant B
C:Genetics:
A:Note: U24

Query Match 4.1%; Score 7; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 PRTPPS 103
|||||
DB 4 PRTPPS 10

RESULT 14
T09318
EoLF1 protein - human herpesvirus 6 (strain U1102)
C:Species: human herpesvirus 6
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T09318
R:Nicholas, J.; Martin, M.
J. Virol. 68, 597-610, 1994
A:Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hu
A:Reference number: Z16644; MUID:94118404
A:Accession: T09318
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-93 <NIC>
A:Cross-references: EMBL:L25528; NID:g451937; PID:g451949
C:Genetics:

A:Gene: EoLF1

Query Match 4.1%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 PRTPPS 103
|||||
DB 10 PRTPPS 16

RESULT 15
A69884
cell wall protein homolog ymag - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: A69884
R:Kunst, F.; Ogatawa, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Boulanger, D.; Fritze, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
lechi, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
Koettler, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, K.; Yasunoto, K.; Yata, K.; Yoshida
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Dancho, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033
A:Accession: A69884
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1-123 <KUN>
A:Cross-references: GB:299113; GB:AL009126; NID:g2634090; PIDN:CAB13615.1; PID:el1833
A:Experimental source: strain 168
C:Genetics:
A:Gene: ymag

Query Match 4.1%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 123 RPFGRG 129
|||||
DB 71 RPFGRG 77

Search completed: September 26, 2000, 19:37:20
Job time: 166 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2000, 19:36:23 ; Search time 7.44 Seconds.

(without alignments)
712.250 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171

Sequence: 1 MASQKRPGRHSGKYLATAS.....SKIFKLGDRSGSGPMARR 171

Scoring table: OLIGO

Searched: 85661 seqs, 30989116 residues

Word size: 0

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	66.1	196	1 MBP_HUMAN	P02686 homo sapien
2	76	44.4	171	1 MBP_PANTR	P06906 pan troglod
3	46	26.9	167	1 MBP_CAVPO	P25188 cavia porce
4	45	26.3	127	1 MBP_RAT	P02688 rattus norv
5	45	26.3	194	1 MBP_MOUSE	P04370 mus musculu
6	41	24.0	169	1 MBP_BOVIN	P02687 bos taurus
7	41	24.0	171	1 MBP_PIG	P01558 sus scrofa
8	12	7.0	42	1 MBP_RABIT	P15274 oryctolagus
9	12	7.0	173	1 MBP_CHICK	P15720 gallus gall
10	8	4.7	154	1 MBP_RAUER	P01325 raja erinac
11	8	4.7	154	1 MBP_SQVAC	P01435 squalus aca
12	8	4.7	323	1 PCP3_AMPCA	P00483 amphidinulu
13	7	4.1	154	1 MBP_HETFR	P20939 heterodontu
14	7	4.1	368	1 YG3V_YEAST	P53295 saccharomyc
15	7	4.1	481	1 LBP_RAT	P03313 rattus norv
16	7	4.1	508	1 EXON_HSVB	P28919 equine hepr
17	7	4.1	532	1 SATT_HUMAN	P43007 homo sapien
18	7	4.1	573	1 YKX3_CAEEL	P42480 caenorhabd1
19	7	4.1	1345	1 VCAP_HSV7J	P23247 herpes simp
20	7	4.1	3305	1 APLP_MANSE	P05049 menduca sex
21	6	3.5	88	1 CUV70_LOCHI	P00233 locusta mig
22	6	3.5	112	1 H34_STYLE	P01198 stylynychia
23	6	3.5	112	1 OLF9_MOUSE	P06088 mus musculu
24	6	3.5	116	1 AON3_PIG	P40200 sus scrofa
25	6	3.5	124	1 YIC5_YEAST	P40542 sus scrofa
26	6	3.5	134	1 YNBL_SYND7	P35086 synchococc
27	6	3.5	148	1 YOR1_HSVB	P08108 bovine hepr
28	6	3.5	150	1 EXON_PRVN3	P30660 pseudorale
29	6	3.5	155	1 YKFB_ECOLI	P77166 escherichia
30	6	3.5	156	1 RR7_MAYSA	P12339 zea mays (m
31	6	3.5	156	1 RR7_ORYSA	P15424 oryza sativ
32	6	3.5	184	1 TRIS_RABIT	P02645 oryctolagus
33	6	3.5	185	1 PHNN_ECOLI	P16690 escherichia

ALIGNMENTS

RESULT 1	MBP_HUMAN	STANDARD;	PRT;	196 AA.
ID	MBP_HUMAN			
AC	P02686;			
DT	21-JUL-1986 (Rel. 01, Created)			
DI	01-NOV-1991 (Rel. 20, last sequence update)			
DI	15-FEB-2000 (Rel. 39, last annotation update)			
DE	MYELIN BASIC PROTEIN (MBP).			
GN	MBP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 89302693.			
RA	Streicher R., Stoffel W.;			
RT	"The organization of the human myelin basic protein gene. Comparison			
RL	with the mouse gene.";			
RL	Biol. Chem. Hoppe-Seyler 370:503-510(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87311781.			
RA	Roth H.J., Kronquist K.E., de Rosbo N., Crandall B.F.,			
RT	"Evidence for the expression of four myelin basic protein variants in			
RL	the developing human spinal cord through cDNA cloning.";			
RL	J. Neurosci. Res. 17:321-328(1987).			
RN	[3]			
RP	SEQUENCE OF 1-58; 85-131 AND 143-196 FROM N.A.			
RX	MEDLINE; 86308101.			
RA	Roth H.J., Kronquist K.E., Pretorius P.J., Crandall B.F.,			
RT	"Isolation and characterization of a cDNA coding for a novel human			
RL	17.3k myelin basic protein (MBP) variant.";			
RL	J. Neurosci. Res. 16:227-238(1986).			
RN	[4]			
RP	SEQUENCE OF 1-58 AND 85-196 FROM N.A.			
RX	MEDLINE; 86259714.			
RA	Kamholz J., de Ferreira F., Puckett C., Lazzarini R.A.;			
RT	"Identification of three forms of human myelin basic protein by cDNA			
RL	cloning.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:4962-4966(1986).			
RN	[5]			
RP	SEQUENCE OF 1-58 AND 85-196.			
RX	MEDLINE; 72066400.			
RA	Carnegele P.R.;			
RT	"Amino acid sequence of the encephalitogenic basic protein from human			
RL	myelin.";			
RL	Biochem. J. 123:57-67(1971).			
RN	[6]			
RP	SEQUENCE OF 45-58 AND 85-114, AND REVISIONS.			
RA	Shapira R., McKenally S.S., Chou F., Kibler R.F.;			
RT	"Encephalitogenic fragment of myelin basic protein. Amino acid			
RL	sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";			
RL	J. Biol. Chem. 246:4630-4640(1971).			
RN	[7]			

34	6	3.5	186	1 TRIS_HUMAN	P19237 homo sapien
35	6	3.5	186	1 TRIS_RAT	P13413 rattus norv
36	6	3.5	206	1 ALAI_MOUSE	P063805 mus musculu
37	6	3.5	214	1 DCOB_THEAC	P29950 thermoplasm
38	6	3.5	217	1 UNG_PSEDE	P29950 pseudomonas
39	6	3.5	225	1 Y638_MENJA	P58055 methanococc
40	6	3.5	244	1 FNRA_PSEST	P47200 pseudomonas
41	6	3.5	249	1 YBFT_BACSU	P01458 bacillus su
42	6	3.5	249	1 YDD1_SCHPO	P10426 schizosacch
43	6	3.5	251	1 TPIS_COPCI	P12574 coprinus ci
44	6	3.5	251	1 YAT8_SCHPO	P01533 schizosacch
45	6	3.5	253	1 CHIO_TOBAC	P17514 nicotiana t

RP SEQUENCE OF 1-58 FROM N.A.
 RX MEDLINE: 90152679.
 RA Boylan K.B., Ayres T.M., Popko B., Takahashi N., Hood L.E.,
 RA Prusiner S.B.;
 RT "Repetitive DNA (TGCA)n 5' to the human myelin basic protein gene: a
 RT new form of oligonucleotide repetitive sequence showing length
 RT polymorphism".
 RL Genomics 6:16-22(1990).
 RN [8]
 RP METHYLATION.
 RX MEDLINE: 72066401.
 RA Baldwin G.S., Carnegie P.R.;
 RT "Isolation and partial characterization of methylated arginines from
 RT the encephalitogenic basic protein of myelin".
 RL Biochem. J. 123:69-74(1971).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- ALTERNATIVE PRODUCTS: THREE ISOFORMS: 21.5 KDA (SHOWN HERE), 18.5
 CC KDA (THE MOST ABUNDANT) AND 17.2 KDA; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: M1577; AAA59562.1; -
 DR EMBL: M30516; AAA59563.1; -
 DR EMBL: M30515; AAA59564.1; -
 DR EMBL: M30047; AAA59559.1; -
 DR EMBL: X17286; CAA35179.1; -
 DR EMBL: X17287; CAA35179.1; JOINED.
 DR EMBL: X17280; CAA35179.1; JOINED.
 DR EMBL: X17288; CAA35179.1; JOINED.
 DR EMBL: X17369; CAA35179.1; JOINED.
 DR EMBL: X17289; CAA35179.1; JOINED.
 DR EMBL: M63599; AAA59560.1; -
 DR PIR: A24153; MBHUB.
 DR PIR: S10482; S10482.
 DR MIM: 159430; -
 DR PFM: PFM169; Myelin_MBP; 1.
 DR PRINTS: PRO0212; MYELINMBP.
 DR PROSITE: PS00569; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 FT INT_MET 0 0
 FT MOD_RES 1 1
 FT MOD_RES 133 133
 FT DOMAIN 45 114
 FT
 FT DOMAIN 138 148
 FT
 FT DOMAIN 59 84
 FT
 FT VARSPLIC 132 142
 FT VARSPLIC 196 AA; 21362 MW; 238BD0C1CE689653 CRC64;
 FT SEQUENCE

Query Match 66.1%; Score 113; DB 1; Length 196;
 Best Local Similarity 100.0%; Pred. No. 2.6e-111;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 59 KDSHNPARTAHYGSLSPOKSHGRTQDENPVVHFKNITVPTPTPPSGKGKGLSLSPFSG 118
 DB 84 KSHNPARTAHYGSLSPOKSHGRTQDENPVVHFKNITVPTPTPPSGKGKGLSLSPFSG 143
 OY 119 ASQGRPGFGYGGASDYKSAHKGFKGVDAQGLTSLFKLGGGRDSGSPMARR 171

DB 144 AEGQRPFGYGGASDYKSAHKGFKGVDAQGLTSLFKLGGGRDSGSPMARR 196
 RESULT 2
 MBP_PANTR
 ID MBP_PANTR STANDARD; PRT; 171 AA.
 AC P06506;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 RN [1]
 RP PRELIMINARY SEQUENCE.
 RX MEDLINE: 76009821.
 RA Westall F.C., Thompson M., Kalter S.S.;
 RT "The proposed sequence of the encephalitogenic protein from
 RT chimpanzee brain."
 RL Life Sci. 17:219-223(1975).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC PIR: A03139; MRC2B.
 DR PFM: PFM169; Myelin_MBP; 1.
 DR PRINTS: PRO0212; MYELINMBP.
 DR PROSITE: PS00569; MYELIN_MBP; 1.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis.
 FT MOD_RES 1 1
 FT MOD_RES 107 107
 FT MOD_RES 171 AA; 18560 MW; E9FED59D6933293 CRC64;
 FT SEQUENCE

Query Match 44.4%; Score 76; DB 1; Length 171;
 Best Local Similarity 100.0%; Pred. No. 1.8e-72;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASQKRPDSQSHGKYLATSTMDHARHGFPRHRDGIIDSLREFGGRGAPKRSKGS 61
 DB 1 ASQKRPDSQSHGKYLATSTMDHARHGFPRHRDGIIDSLREFGGRGAPKRSKGS 60
 OY 62 HNPARTAHYGSLSPOKS 77
 DB 61 HNPARTAHYGSLSPOKS 76

RESULT 3
 MBP_CAVPO
 ID MBP_CAVPO STANDARD; PRT; 167 AA.
 AC P25188;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN Cavia porcellus (Guinea pig).
 OS Eukaryota; Metazoa; Chordata;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 84215086.
 RA Delbier G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;
 RT "Sequence of guinea pig myelin basic protein."
 RL J. Neurochem. 43:100-105(1984).
 RN [2]
 RP SEQUENCE OF 45-87.
 RA Shapiro R., McKenally S.S., Chou F., Kibler R.F.;
 RT "Encephalitogenic fragment of myelin basic protein. Amino acid
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments."

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CC CC SMALLER ONE, SHOWN HERE, IS MISSING 40 RESIDUES (FOLLOWING RESIDUE
CC CC 113 OR 114) WITH RESPECT TO THE LARGER ONES FROM OTHER SPECIES.
CC CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; M25889; AAA41575.1; "-
DR DR EMBL; K00512; "- NOT_ANNOTATED_CDS.
DR DR PIR; A03142; MBPTS.
DR DR PIR; B24351; B24351.
DR DR PIR; A21062; A21062.
DR DR PIR; PFO1669; Myelin_MBP; 1.
DR DR PROSITE; PRO0212; MYELINMBP.
DR DR PROSITE; PS00569; MYELINMBP; 1.
KW KW Myelin; structural protein; Acetylation; Methylation; Phosphorylation;
KW Autoimmune encephalomyelitis; Alternative splicing.
FT FT INIT_MBT 0 0
FT FT MOD_RES 1 1 ACETYLATION.
FT FT MOD_RES 104 104 METHYLATION (MONO-:44% OR DI-:11%).
FT FT CONFLICT 46 47 SG -> GS (IN REF. 4).
FT FT CONFLICT 124 124 M -> I (IN REF. 2).
SQ SQ SEQUENCE 127 AA; 14080 MW; B4C9F33C19A9E137 CRC64;

Query Match 26.3%; Score 45; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 5,1e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ASQKRPQSQRHSGSKYLATASTMDHARHGFLPHRRDGTGIDSGRFF 45
DB 1 ASQKRPQSQRHSGSKYLATASTMDHARHGFLPHRRDGTGIDSGRFF 45

RESULT 5
MBP_MOUSE
ID MBP_MOUSE STANDARD; PRT; 194 AA.
AC P04370;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP).
GN MBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN RP SEQUENCE FROM N.A. (ALL FOUR FORMS).
RAX MEDLINE; 86079555.
RA de Ferra F., Engh H., Hudson L., Kamholz J., Puckett C., Molinaux S.,
RA lazzarini R.A.;
RT "Alternative splicing accounts for the four forms of myelin basic
RT protein.";
RL Cell 43:721-727(1985).
RN [2]
RN RP SEQUENCE FROM N.A. (18.5 KDA FORM).
RAX MEDLINE; 85254913.
RA Takahashi N., Roach A., Teplov D.B., Frustier S.B., Hood L.;
RT "Cloning and characterization of the myelin basic protein gene from
RT mouse: one gene can encode both 14 kd and 18.5 kd MBPs by alternate
RT use of exons.";
RL Cell 42:139-148(1985).
RN [3]
RN RP SEQUENCE FROM N.A. (17 KDA FORM).
RAX MEDLINE; 87118269.
RA Newman S., Kitamura K., Campagnoni A.T.;
RT "Identification of a cDNA coding for a fifth form of myelin basic
RT protein in mouse.";

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RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).
 RN [4]
 RP SEQUENCE OF 1-23 FROM N.A.
 RX MEDLINE: 89252919.
 RT Mura M., Tamura T.A., Aoyama A., Mtkoshba K.;
 RT "The promoter elements of the mouse myelin basic protein gene
 RT function efficiently in NG108-15 neuronal/gliai cells.";
 RT Gene 75:31-38(1989).
 RL CC
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- ALTERNATIVE PRODUCTS: FOUR ISOFORMS: 21.5 KDA (SHOWN HERE), 18.5
 CC KDA, 17 KDA AND 14 KDA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
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 CC
 DR EMBL: M11533: AAA39496.1: -
 DR EMBL: M11291: AAA39496.1: JOINED.
 DR EMBL: M11528: AAA39496.1: JOINED.
 DR EMBL: M11530: AAA39496.1: JOINED.
 DR EMBL: M11531: AAA39496.1: JOINED.
 DR EMBL: M11532: AAA39496.1: JOINED.
 DR EMBL: M11533: AAA39496.1: JOINED.
 DR EMBL: M11291: AAA39497.1: JOINED.
 DR EMBL: M11528: AAA39497.1: JOINED.
 DR EMBL: M11530: AAA39497.1: JOINED.
 DR EMBL: M11531: AAA39497.1: JOINED.
 DR EMBL: M11532: AAA39497.1: JOINED.
 DR EMBL: M11533: AAA39497.1: JOINED.
 DR EMBL: L00398: AAA39499.1: JOINED.
 DR EMBL: L00400: AAA39499.1: JOINED.
 DR EMBL: L00401: AAA39499.1: JOINED.
 DR EMBL: L00402: AAA39499.1: JOINED.
 DR EMBL: L00403: AAA39499.1: JOINED.
 DR EMBL: L00404: AAA39500.1: JOINED.
 DR EMBL: L00398: AAA39500.1: JOINED.
 DR EMBL: L00399: AAA39500.1: JOINED.
 DR EMBL: L00400: AAA39500.1: JOINED.
 DR EMBL: L00401: AAA39500.1: JOINED.
 DR EMBL: L00402: AAA39500.1: JOINED.
 DR EMBL: L00403: AAA39500.1: JOINED.
 DR EMBL: L00404: AAA39500.1: JOINED.
 DR EMBL: L00398: AAA39501.1: JOINED.
 DR EMBL: L00399: AAA39501.1: JOINED.
 DR EMBL: L00400: AAA39501.1: JOINED.
 DR EMBL: L00401: AAA39501.1: JOINED.
 DR EMBL: L00402: AAA39501.1: JOINED.
 DR EMBL: L00403: AAA39501.1: JOINED.
 DR EMBL: L00404: AAA39501.1: JOINED.
 DR EMBL: L00398: AAA39502.1: JOINED.
 DR EMBL: L00399: AAA39502.1: JOINED.
 DR EMBL: L00400: AAA39502.1: JOINED.
 DR EMBL: L00401: AAA39502.1: JOINED.
 DR EMBL: L00402: AAA39502.1: JOINED.
 DR EMBL: L00403: AAA39502.1: JOINED.
 DR EMBL: L00404: AAA39502.1: JOINED.
 DR EMBL: L00403: AAA39502.1: JOINED.
 DR EMBL: L00404: AAA39502.1: JOINED.
 DR EMBL: M24410: AAA39498.1: -
 DR PIR: A24772: MEMSB.
 DR PIR: A26591: A26591.
 DR PIR: B26591: B26591.
 DR MGD: MGI:96925: MBP.
 DR PRAM: PFO1669: Myelin_MBP. 1.
 DR PRINTS: PRO0212: MYELINMBP.
 DR PROSITE: PS00569: MYELIN_MBP. 1.
 DR Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 KM Autoimmune encephalomyelitis; Alternative splicing.
 FT INIT_MET 0 0
 FT MOD_RES 1 130 ACETYLATION (BY SIMILARITY).
 FT VARSPIC 57 82 METHYLATION (BY SIMILARITY).
 FT MISSING (IN 18.5 KDA ISOFORM AND 14 KDA

FT FT ISOFORM).
 FT VARSPIC 140 180 MISSING (IN 17 KDA ISOFORM AND 14 KDA
 FT FT ISOFORM).
 SQ SEQUENCE 194 AA: 21371 MW; D208CACOCF52ACD2 CRC64;
 Query Match 26.3%; Score 45; DB 1; Length 194;
 Best Local Similarity 100.0%; Pred. No. 7.4e-40;
 Matches 45; Conservative 0; Mismatches 0; Gaps 0;
 OY 78 HGRDQENPVVHFKNIVPTPTPPSGRGSLSRFSWGAEGQ 122
 DB 100 HGRDQENPVVHFKNIVPTPTPPSGRGSLSRFSWGAEGQ 144
 RESULT 6
 ID MBP_BOVIN STANDARD; PRT; 169 AA.
 AC P02687;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP) (MYELIN A1 PROTEIN).
 GN Bos.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 72007306.
 RA Eylar E.H., Brostoff S.W., Hashin G., Caccam J., Burnett P.;
 RT "Basic A1 protein of the myelin membrane. The complete amino acid
 RT sequence.";
 RL J. Biol. Chem. 246:5770-5784(1971).
 RN [2]
 RP REVISION.
 RX MEDLINE: 74070688.
 RA Brostoff S.W., Reuter W., Hichens M., Eylar E.H.;
 RT "Specific cleavage of the A1 protein from myelin with cathepsin D.";
 RL J. Biol. Chem. 249:559-567(1974).
 RN [3]
 RP SEQUENCE OF 43-87.
 RA Shapira R., McKneally S.S., Chou F., Kibler R.F.;
 RT "Encephalitic fragment of myelin basic protein. Amino acid
 RT sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";
 RL J. Biol. Chem. 246:4630-4640(1971).
 RN [4]
 RP METHYLATION.
 RX MEDLINE: 71153946.
 RA Brostoff S.W., Eylar E.H.;
 RT "Localization of methylated arginine in the A1 protein from myelin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).
 RN [5]
 RP SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING REGION.
 RX MEDLINE: 70178977.
 RA Eylar E.H., Caccam J., Jackson J.J., Westall F.C., Robinson A.B.;
 RT "Experimental allergic encephalomyelitis: synthesis of
 RT disease-inducing site of the basic protein.";
 RL Science 168:1220-1223(1970).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
 CC PIR: A03140: MBP.
 DR PRAM: PFO1669: Myelin_MBP. 1.
 DR PRINTS: PRO0212: MYELINMBP.
 DR PROSITE: PS00569: MYELIN_MBP. 1.
 DR Myelin: Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis.
 KM Autoimmune encephalomyelitis.
 FT MOD_RES 1 106 ACETYLATION.
 FT MOD_RES 106 106 METHYLATION (MONO- OR DI-).
 FT DOMAIN 114 122 INDUCES EXPERIMENTAL AUTOIMMUNE

FT SEQUENCE 169 AA: 18323 MW: 8E1157B7A1978484 CRC64: ENCEPHALOMYELITIS

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 169;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 ODENVVHFFKNIVTPRPPPSQGGKRGSLSRFSWGAEQ 122
DB 80 ODENVVHFFKNIVTPRPPPSQGGKRGSLSRFSWGAEQ 120

RESULT 7
MBP_PIG ID MBP_PIG STANDARD: PRT; 171 AA.

AC P81558;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP).
GN MBP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE.
RC TISSUE-BRAIN;
RX MEDLINE; 85056964.
RA Ira J. -, Delbler G. E., Krutzsch H. C., Martenson R. E.;
RT "Amino acid sequence of porcine myelin basic protein.";
RL J. Neurochem. 44:134-142(1985).
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KM Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
FT MOD_RES 1 1 ACETYLATION.
FT MOD_RES 107 1 METHYLATION (MONO- OR DI-) (BY
FT MOD_RES 107 107 SIMILARITY)
FT DOMAIN 115 123 INDUCES EXPERIMENTAL AUTOIMMUNE
FT SEQUENCE 171 AA: 18487 MW: 287AEDF2F24028D9 CRC64; ENCEPHALOMYELITIS (BY SIMILARITY).

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 171;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 ODENVVHFFKNIVTPRPPPSQGGKRGSLSRFSWGAEQ 122
DB 81 ODENVVHFFKNIVTPRPPPSQGGKRGSLSRFSWGAEQ 121

RESULT 8
MBP_RABIT ID MBP_RABIT STANDARD: PRT; 42 AA.

AC P25274;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-FEB-2000 (Rel. 39, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP) (MYELIN AL PROTEIN) (FRAGMENT).
GN MBP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RA Shastra R., McNeally S. S., Chou F., Kibler R. F.;
RT "Encephalogenic fragment of myelin basic protein. Amino acid
sequence of bovine, rabbit, guinea pig, monkey, and human fragments.";

RL J. Biol. Chem. 246:4630-4640(1971).
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
DR PROSITE; PS00569; MYELIN_MBP; PARTIAL.
KM Myelin; Structural protein; Autoimmune encephalomyelitis.
FT NON_TER 1 1
FT NON_TER 42 42
SQ SEQUENCE 42 AA: 4537 MW: E283198F53F6DE73 CRC64;

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 42;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 DRGAPKRGSGKD 60
DB 4 DRGAPKRGSGKD 15

RESULT 9
MBP_CHICK ID MBP_CHICK STANDARD: PRT; 173 AA.

AC P15720;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE MYELIN BASIC PROTEIN (MBP).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE; LEEHORN; TISSUE-BRAIN;
RX MEDLINE; 89358239.
RA Zopf D., Sonntag H., Betz H., Gundelfinger E. D.;
RT "Developmental accumulation and heterogeneity of myelin basic protein transcripts in the chick visual system.";
RL Glia 2:241-249(1989).
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL; X17103; CAA34959.1; -.
DR PIR; S08535; S08535.
DR PIR; P01669; Myelin_MBP; 1.
DR PRINTS; PR00212; MYELIN_MBP; 1.
DR PROSITE; PS00569; MYELIN_MBP; 1.
KM Myelin; Structural protein; Acetylation; Methylation; Phosphorylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT MOD_RES 105 105 METHYLATION (BY SIMILARITY).
FT SEQUENCE 173 AA: 18677 MW: ABEF70D4C9CF019D CRC64;

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 173;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 OGTLKIRKLG 159
DB 148 OGTLKIRKLG 159

Db 146 OGTLKFKLGG 157

RESULT 10

ID MBP_RAJER STANDARD; PRT; 154 AA.

AC 091325;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE MYELIN BASIC PROTEIN (MBP).

GN MBP.

OS Raja erinacea (Little skate).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Neoselachii; Squalae; Hypnosqualae; Pristigastera;

OC Batoidae; Rajiformes; Rajidae; Rajae; Raja.

[1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN, AND SPINAL CORD;

RX MEDLINE; 94016687.

RA SPIVACK W.D., Zhong N., Salerno S., Saavedra R.A., Gould R.M.;

RT Molecular cloning of the myelin basic proteins in the shark, Squalus

acanthias, and the ray, Raja erinacea."

RL J. Neurosci. Res. 35:577-584(1993).

CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE

OF MYELIN.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.

CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.

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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SKYLATAS 20
|||||

Db 204 SKYLATAS 211

RESULT 13

MBP_HETFR STANDARD; PRT; 154 AA.

ID MBP_HETFR

AC P20939;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE MYELIN BASIC PROTEIN (MBP).

OS Heterodontus francisci (Horn shark).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

OC Elasmobranchii; Neoselachii; Galeomorphii; Heterodontoidae;

OC Heterodontiformes; Heterodontidae; Heterodontus.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE: 90040744.

RA Sanders J., Hood L., Abersold R.H., Arden B., Horvath S.,

RT "The myelin proteins of the shark brain are similar to the myelin

RT proteins of the mammalian peripheral nervous system."

RL J. Mol. Evol. 29:149-156(1989).

CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE

CC OF MYELIN.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.

CC -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.

CC -----

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CC -----

DR EMBL: X17664; CA35661.1; -

DR PIR: B32999; B32999.

DR PRAM: PFO1669; Myelin_MBP; 1.

DR PRINTS: PRO0212; MYELINMBP.

DR PROSITE: PS00569; MYELIN_MBP; 1.

KM Myelin, structural protein; Acetylation; Phosphorylation.

FT INT_MET 0 0 BY SIMILARITY.

FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

SQ SEQUENCE 154 AA; 16502 MW; A9A57DA149429A83 CRC64;

Query Match 4.1%; Score 7; DB 1; Length 154;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 VVHEFFKN 93
|||||

Db 74 VVHEFFKN 80

RESULT 14

YGY3_YEAST STANDARD; PRT; 368 AA.

ID YGY3_YEAST

AC P53295;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-1999 (Rel. 38, Last annotation update)

DE HYPOTHEICAL 41.0 KDA PROTEIN IN YIP1-CBP4 INTERGENIC REGION.

GN YG173M.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]

RP SEQUENCE FROM N.A.

RA Hebling U., Hofmann B., Delius H.;

RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE GTP1/ORG FAMILY.

CC -----

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CC -----

DR EMBL: Z72958; CA97199.1; -

DR PRAM: PFO1018; GTP1_ORG; 1.

DR PRINTS: PRO0326; GTP1_ORG.

DR PROSITE: PS00905; GTP1_ORG; 1.

KM Hypothetical protein; GTP-binding.

FT NP_BIND 70 77 GTP (BY SIMILARITY).

FT NP_BIND 116 120 GTP (BY SIMILARITY).

FT NP_BIND 250 253 GTP (BY SIMILARITY).

SQ SEQUENCE 368 AA; 41006 MW; D144569C9C5D777C CRC64;

Query Match 4.1%; Score 7; DB 1; Length 368;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 SQGKRG 109
|||||

Db 125 SQGKRG 131

RESULT 15

LBP_RAT STANDARD; PRT; 481 AA.

ID LBP_RAT

AC 063313;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP).

GN LBP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;

RX MEDLINE: 94292804.

RA Su G.L., Freeswick P.D., Geller D.A., Wang Q., Shapiro R.A., Wan Y.H.,

RT "Molecular cloning, characterization, and tissue distribution of rat

RT lipopolysaccharide binding protein. Evidence for extraneuphatic

RT expression."

RT J. Immunol. 153:743-752(1994).

CC -1- FUNCTION: BINDS TO THE LIPID A MOIETY OF BACTERIAL

CC LIPOPOLYSACCHARIDES (LPS), A GLYCOLIPID PRESENT IN THE OUTER

CC MEMBRANE OF ALL GRAM-NEGATIVE BACTERIA. THE LBP/LPS COMPLEX SEEMS

CC TO INTERACT WITH THE CD14 RECEPTOR.

CC -1- SIMILARITY: BELONGS TO THE BPI/CEP/LBP/PLTP FAMILY.

CC -----

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CC -----

DR EMBL: L32133; AAA21835.1; -

DR HSSP: P17213; LBPI.

DR PFAM; PF01273; LBP_BPI_CETP; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
KW Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 481 LIPOLYSACCHARIDE-BINDING PROTEIN.
FT CARBOHYD 300 300 POTENTIAL.
FT CARBOHYD 355 355 POTENTIAL.
SQ SEQUENCE 481 AA; 53600 MW; 23E67CB9CC97D2FC CRC64;

Query Match 4.1%; Score 7; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 GRGLSL 113
Db 98 GRGLSL 104

Search completed: September 26, 2000, 19:38:14
Job time: 111 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: September 26, 2000, 19:36:43 ; Search time 13.52 Seconds

(without alignments)
876.933 Million cell updates/sec

Title: US-09-218-277-12

Perfect score: 171

Sequence: 1 MASOKRPSQHRGSKYLATAS.....SKIFKUGRDSRSGSPMARR 171

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 225878 seqs, 69334122 residues

Word size : 0

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL.12.*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	171	100.0	304	4 Q15340	Q15340 homo sapien
2	59	34.5	197	4 Q15339	Q15339 homo sapien
3	46	26.9	154	11 Q92106	Q92106 rattus norv
4	46	26.9	169	11 Q92105	Q92105 rattus norv
5	46	26.9	195	11 Q92104	Q92104 rattus norv
6	34	19.9	149	11 Q61836	Q61836 mus musculu
7	34	19.9	195	11 Q01585	Q01585 mus musculu
8	34	19.9	250	11 Q03139	Q03139 mus musculu
9	17	9.9	34	11 Q61837	Q61837 mus musculu
10	8	4.7	176	13 P87346	P87346 xenopus lae
11	8	4.7	281	10 Q38690	Q38690 amphidinlum
12	7	4.1	87	12 Q69559	Q69559 human herpe
13	7	4.1	88	12 Q9W140	Q9W140 human herpe
14	7	4.1	93	12 Q69048	Q69048 human herpe
15	7	4.1	123	2 Q31793	Q31793 bacillus su
16	7	4.1	140	10 Q9XFE2	Q9XFE2 oryza sativ
17	7	4.1	259	5 Q21174	Q21174 caenorhabdi
18	7	4.1	259	12 Q98438	Q98438 paramacrum
19	7	4.1	332	2 Q67104	Q67104 aquifex ae

20	7	4.1	364	13 Q57346	Q57346 oncorhynch
21	7	4.1	545	10 Q80750	Q80750 arabidopsis
22	7	4.1	565	12 Q39290	Q39290 equine herp
23	7	4.1	813	2 Q87964	Q87964 thermotoga
24	7	4.1	1151	13 Q57580	Q57580 gallus gall
25	7	4.1	1344	12 Q69071	Q69071 human herpe
26	6	3.5	45	12 Q39703	Q39703 polyomaviru
27	6	3.5	59	13 Q91419	Q91419 gallus gall
28	6	3.5	71	12 Q12311	Q12311 hepatitis g
29	6	3.5	72	2 Q66174	Q66174 agrobacteri
30	6	3.5	72	2 Q92484	Q92484 agrobacteri
31	6	3.5	89	4 Q43185	Q43185 homo sapien
32	6	3.5	96	2 Q51168	Q51168 borrelia bu
33	6	3.5	102	3 Q12047	Q12047 saccharomyc
34	6	3.5	103	12 Q55294	Q55294 hepatitis g
35	6	3.5	103	12 Q55295	Q55295 hepatitis g
36	6	3.5	103	12 Q55299	Q55299 hepatitis g
37	6	3.5	103	12 Q55303	Q55303 hepatitis g
38	6	3.5	103	12 Q55310	Q55310 hepatitis g
39	6	3.5	103	12 Q55311	Q55311 hepatitis g
40	6	3.5	103	12 Q55314	Q55314 hepatitis g
41	6	3.5	103	12 Q55316	Q55316 hepatitis g
42	6	3.5	104	10 Q42244	Q42244 arabidopsis
43	6	3.5	109	2 Q9X292	Q9X292 thermotoga
44	6	3.5	111	12 Q82080	Q82080 hirtane thab
45	6	3.5	111	13 Q9YH66	Q9YH66 brachydanio

ALIGNMENTS

RESULT 1
ID Q15340 PRELIMINARY: PRT: 304 AA.
AC Q15340:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GOLTI-MBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euthera; Primates; Catarrhini; Hominoidea; Homo.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94068468.
RA PRIEVL T.M., CAMPAGNONI C.W., KAMPE K., KASHIMA T., HANDLEY V.W.,
RA MCNAHON J., CAMPAGNONI A.T.;
RA "The human myelin basic protein gene is included within a 179-Kilobase
RT transcription unit: expression in the immune and central nervous
RT systems.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10695-10699(1993).
DR EMBL: L18866; AAA72011.1.;
DR PROSITE: PS00569; MYELINMBP.
DR PRINTS: PR00212; MYELINMBP.
SQ SEQUENCE 304 AA; 33117 MW; 4E98B0AE CRC32;

Query Match 100.0%; Score 171; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 4.0e-175;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASOKRPSQHRGSKYLATASMTDHRHGHGFLPRHRTGILDSIGRFEGDGRGAPKRGSGMD 60
DB 134 MASOKRPSQHRGSKYLATASMTDHRHGHGFLPRHRTGILDSIGRFEGDGRGAPKRGSGMD 193
QY 61 SHHPRATAHYGLPKSHGRGTODENPVVHFFKNITVPTPTPPSQGKRGSLSTRFSWGAE 120
DB 194 SHHPRATAHYGLPKSHGRGTODENPVVHFFKNITVPTPTPPSQGKRGSLSTRFSWGAE 253
QY 121 GRRPFGVGGGRASDYKSAHKGFKGVDAOGTSLKTKLGGDRSGSPMARR 171
DB 254 GRRPFGVGGGRASDYKSAHKGFKGVDAOGTSLKTKLGGDRSGSPMARR 304

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DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE MYELIN BASIC PROTEIN.
GN MBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LEWIS RAT.
RA LOBELLI A.M.; WIGZELL H.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ132897; CAAL0806.1; -.
SQ PROSITE; PS00569; MYELIN_MBP; 1.
SO SEQUENCE 169 AA; 18470 MW; B0A/C0A0 CRC32;

RESULT 5
Query Match 26.9%; Score 46; DB 11; Length 169;
Best Local Similarity 100.0%; Pred. No. 2.1e+11;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MASOKRPSQRHSGKYLTASTMDARHGFLPRHDTGILDSIGRF 46
|||||
1 MASOKRPSQRHSGKYLTASTMDARHGFLPRHDTGILDSIGRF 46

RESULT 5
ID Q92I14 PRELIMINARY; PRT; 195 AA.
AC Q92I14;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DI 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE MYELIN BASIC PROTEIN.
GN MBP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LEWIS RAT.
RA LOBELLI A.M.; WIGZELL H.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ132898; CAAL0807.1; -.
SQ PROSITE; PS00569; MYELIN_MBP; 1.
SO SEQUENCE 195 AA; 21484 MW; 79E52D9D CRC32;

Query Match 26.9%; Score 46; DB 11; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.3e+11;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASOKRPSQRHSGKYLTASTMDARHGFLPRHDTGILDSIGRF 46
|||||
1 MASOKRPSQRHSGKYLTASTMDARHGFLPRHDTGILDSIGRF 46

Db 1 MASOKRPSQRHSGKYLTASTMDARHGFLPRHDTGILDSIGRF 46

RESULT 6
ID Q61836 PRELIMINARY; PRT; 149 AA.
AC Q61836;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DI 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE MYELIN BASIC PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-BRAIN.
RX MEDLINE; 87118269.
TX NEWMAN S., KITAHARA K., CAMPAGNONI A.T.;
TY Identification of a cDNA coding for a fifth form of myelin basic

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RT protein in mouse."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:886-890(1987).
 DR EMBL; M15062; AAB59712.1; -;
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Alternative splicing; Myelin.
 FT NON TER
 SQ SEQUENCE 149 AA; 16226 MW; A6DC1599 CRC32;

Query Match 19.9%; Score 34; DB 11; Length 149;
 Best Local Similarity 100.0%; Pred. No. 1.3e-28;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 SKYLATASTMDHARHGFLPRHRDTGILDSIGRFF 46
 |||||
 DB 2 SKYLATASTMDHARHGFLPRHRDTGILDSIGRFF 35

RESULT 7

ID 001585 PRELIMINARY; PRT; 195 AA.
 AC 001585;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 GN MBP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57 BL/6J; TISSUE-BONE MARROW;
 RX MEDLINE; 93057537.
 RA GRIMA B., ZELENKA D., PESSAC B.;
 RT "A novel transcript overlapping the myelin basic protein gene.";
 RL J. Neurochem. 59:2318-2323(1992).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-BRAIN;
 RX MEDLINE; 93186801.
 RA CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPE K.,
 RA AMR-DHARSEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBAR B.,
 RA KITAHARA K.;
 RT "Structure and developmental regulation of Goli-mbp, a 105-kilobase
 RT gene that encompasses the myelin basic protein gene and is expressed
 RT in cells in the oligodendrocyte lineage in the brain.";
 RL J. Biol. Chem. 268:4930-4938(1993).
 CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
 CC OF MYELIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
 CC EMBL; X67319; CA44733.1; -;
 DR EMBL; I07508; AAA37721.1; -;
 DR MGD; MGI:96925; MBP
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 SQ SEQUENCE 195 AA; 21004 MW; 557D83EA CRC32;

Query Match 19.9%; Score 34; DB 11; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.6e-28;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 SKYLATASTMDHARHGFLPRHRDTGILDSIGRFF 46
 |||||
 DB 144 SKYLATASTMDHARHGFLPRHRDTGILDSIGRFF 177

RESULT 8

ID 003139 PRELIMINARY; PRT; 250 AA.
 AC 003139;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MYELIN BASIC PROTEIN (MBP).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6; TISSUE-BRAIN;
 RX MEDLINE; 93186801.
 RA CAMPAGNONI A.T., PRIBYL T.M., CAMPAGNONI C.W., KAMPE K.,
 RA AMR-DHARSEE S., LANDRY C., HANDLEY V., NEWMAN S., GARBAR B.,
 RA KITAHARA K.;
 RT "Structure and developmental regulation of Goli-mbp, a 105-kilobase
 RT gene that encompasses the myelin basic protein gene and is expressed
 RT in cells in the oligodendrocyte lineage in the brain.";
 RL J. Biol. Chem. 268:4930-4938(1993).
 DR EMBL; I07507; AAA37720.1; -;
 DR PRINTS; PR00212; MYELINMBP.
 KW Myelin; Structural protein; Acetylation; Methylation; Phosphorylation;
 KW Autoimmune encephalomyelitis; Alternative splicing.
 SQ SEQUENCE 250 AA; 27167 MW; 3A08ADF7 CRC32;

Query Match 19.9%; Score 34; DB 11; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2e-28;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 SKYLATASTMDHARHGFLPRHRDTGILDSIGRFF 46
 |||||
 DB 144 SKYLATASTMDHARHGFLPRHRDTGILDSIGRFF 177

RESULT 9

ID 061837 PRELIMINARY; PRT; 34 AA.
 AC 061837;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE MYELIN BASIC PROTEIN (FRAGMENT).
 GN SHI-MLD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 88186094.
 RA OKANO H., TANURA T., MURA M., AOYAMA A., IKENAKA K., OSHIMURA M.,
 RA MIKOSHIBA K.;
 RT "Gene organization and transcription of duplicated MBP genes of myelin
 RT deficient (shl/mlld) mutant mouse.";
 RL EMBO J. 7:77-83(1988).

DR EMBL; M36275; AAA39504.1; -;
 DR PROSITE; PS00569; MYELIN_MBP; 1.
 KW Myelin.
 FT NON TER
 FT NON TER
 SQ SEQUENCE 34 AA; 3958 MW; 31F53967 CRC32;

Query Match 9.9%; Score 17; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6e-11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 HGRIDENPVVHFFKNI 94
 |||||
 DB 18 HGRIDENPVVHFFKNI 34

RESULT 10

ID P87346 PRELIMINARY; PRT; 176 AA.
 DT P87346

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AC  P87346;
DT  01-MAY-1997 (TEMBLrel. 03, Created)
DT  01-MAY-1997 (TEMBLrel. 03, Last sequence update)
DT  01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE  MYELIN BASIC PROTEIN.
OC  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC  Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae;
OC  Xenopus.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-J; TISSUE-BRAIN;
RA  NAGATA S., OGINO K.;
RT  "CDNA for Xenopus laevis myelin basic protein.";
RL  Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB000736; BA19174.1; -.
DR  PRINTS; PR00212; MYELINBP.
KM  Myelin.
SQ  SEQUENCE 176 AA; 19720 MW; ABF3F06B CRC32;

Query Match 4.7%; Score 8; DB 13; Length 176;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  97 PRTPPSQ 104
    |||||
DB  101 PRTPPSQ 108

RESULT 11
Q38690 ID Q38690 PRELIMINARY; PRT; 281 AA.
AC  Q38690;
DT  01-NOV-1996 (TEMBLrel. 01, Created)
DT  01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT  01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE  HIGH SALT PERIDININ-CHLOROPHYLL A-PROTEIN (FRAGMENT).
OC  Amphidinium carterae (Dinoflagellate).
OC  Eukaryota; Alveolata; Dinophyceae; Gymnodiniales; Gymnodinaceae;
OC  Amphidinium.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CS 21;
RA  SHARPLES F.P., WRENCH P.M., OU K., HILLER R.G.;
RL  Blochim. Biophys. Acta 0:0-0(1996).
DR  EMBL; 271600; CAA96255.1; -.
DR  MENDEL; 16839; Ampca; 2754; 16839.
FT  NON_TER 1 1
FT  NON_TER 281 281
SQ  SEQUENCE 281 AA; 29946 MW; 98FD660F CRC32;

Query Match 4.7%; Score 8; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  13 SKYLATAS 20
    |||||
DB  184 SKYLATAS 191

RESULT 12
Q69559 ID Q69559 PRELIMINARY; PRT; 87 AA.
AC  Q69559;
DT  01-NOV-1996 (TEMBLrel. 01, Created)
DT  01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT  01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE  U24, GLYCOPROTEIN.
GN  U24.
OS  Human herpesvirus 6.
OC  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

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OC  Betaherpesvirinae; Roseolovirus.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 95266321.
RA  GOMPELS U.A., NICHOLAS J., LAWRENCE G., JONES M., THOMSON B.J.,
RA  MARTIN M.E., EFSTATHIOU S., CRAXTON M., MACHULAVI H.A.;
RT  "The DNA sequence of human herpesvirus-6: structure, coding content,
RT  and genome evolution.";
RL  J. Virol. 209:29-51(1995).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 90080132.
RA  LAWRENCE G.L., CHEE M., CRAXTON M.A., GOMPELS U.A., HONESS R.W.,
RA  BARRELL B.G.;
RT  "Human herpesvirus 6 is closely related to human cytomegalovirus.";
RL  J. Virol. 64:287-299(1990).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 91237802.
RA  CHANG C.K., BALACHANDRAN N.;
RT  "Identification, characterization, and sequence analysis of a CDNA
RT  encoding a phosphoprotein of human herpesvirus 6.";
RL  J. Virol. 65:2884-2894(1991).
RN  [4]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 91333007.
RA  TEO I.A., GRIFFIN B.E., JONES M.D.;
RT  Characterization of the DNA polymerase gene of human herpesvirus 6.";
RL  J. Virol. 65:4670-4680(1991).
RN  [5]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 9126542.
RA  THOMSON B.J., EFSTATHIOU S., HONESS R.W.;
RT  "Acquisition of the human adeno-associated virus type-2 rep gene by
RT  human herpesvirus type-6.";
RL  Nature 351:78-80(1991).
RN  [6]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 91374590.
RA  MARTIN M.E.D., NICHOLAS J., THOMSON B.J., NEWMAN C., HONESS R.W.;
RT  "Identification of a transactivating function mapping to the putative
RT  immediate-early locus of human herpesvirus 6.";
RL  J. Virol. 65:5381-5390(1991).
RN  [7]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 92333249.
RA  EFSTATHIOU S., LAWRENCE G.L., BROWN C.M., BARRELL B.G.;
RT  "Identification of homologues to the human cytomegalovirus US22 gene
RT  family in human herpesvirus 6.";
RL  J. Gen. Virol. 73:1661-1671(1992).
RN  [8]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 92146942.
RA  GENG Y., CHANDRAN B., JOSEPHS S.F., WOOD C.;
RT  "Identification and characterization of a human herpesvirus 6 gene 1
RT  promoter.";
RL  J. Virol. 66:1564-1570(1992).
RN  [9]
RP  SEQUENCE FROM N.A.
RC  STRAIN-U1102, VARIANT A;
RX  MEDLINE; 93091236.
RA  GOMPELS U.A., CARSS A.L., SUN N., ARRARD J.R.;
RT  "Infectivity determinants encoded in a conserved gene block of human
RT  herpesvirus-6.";

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RL DNA Seq. 3:25-39(1992).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 92260671.
 RA NEIPEL F., ELLINGER K., FLECKENSTEIN B.;
 RT "Gene for the major antigenic structural protein (p100) of human
 RL J. Virol. 66:3918-3924(1992).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 92333248.
 RA THOMSON B.J., HONESS R.W.;
 RT "The right end of the unique region of the genome of human herpesvirus
 RL J. Gen. Virol. 73:1649-1660(1992).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93187613.
 RA ELLINGER K., NEIPEL F., FOA-TOMASI L., CAMPADDELLI-FITME G.,
 RT "The glycoprotein B homologue of human herpesvirus 6.";
 RL J. Gen. Virol. 74:495-500(1993).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93224882.
 RA GOMPELS U.A., CARRIGAN D.R., CARBS A.L., ARNO J.;
 RT "Two groups of human herpesvirus 6 identified by sequence analyses of
 RL J. Gen. Virol. 74:613-622(1993).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93389439.
 RA LIO D.X., GOMPELS U.A., NICHOLAS J., LELLIOTT C.;
 RT "Identification and expression of the human herpesvirus 6 glycoprotein
 RL J. Gen. Virol. 74:1847-1857(1993).
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 94025558.
 RA LIO D.X., GOMPELS U.A., FOA-TOMASI L., CAMPADDELLI-FITME G.;
 RT "Human herpesvirus-6 glycoprotein H and L homologs are components of
 RL J. Virol. 197:12-22(1993).
 RN [16]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93331710.
 RA PELLET P.E., SANCHEZ-MARTINEZ D., DOMINGUEZ G., BLACK J.B., ANTON E.,
 RT "A strongly immunoreactive virion protein of human herpesvirus 6
 RL J. Virol. 195:521-531(1993).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 93333202.
 RA PELLET P.E., BERENMAN Z.N., NEIPEL F., CHANG C.K., TIRMATNAPONG S.,
 RT "Identification and mapping of the gene encoding the glycoprotein
 RL J. Virol. 67:4611-4620(1993)."

RN [18]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 95146989.
 RA GOMPELS U.A., MACAULAY H.A.;
 RT "Characterization of human telomeric repeat sequences from human
 RL J. Gen. Virol. 76:451-458(1995).
 RN [19]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 94047392.
 RA DEWHURST S., DOLLARD S.C., PELLET P.E., DAMBAUGH T.R.;
 RT "Identification of a lytic-phase origin of DNA replication in human
 RL J. Virol. 67:7680-7683(1993).
 RN [20]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 94118404.
 RA NICHOLAS J., MARTIN M.;
 RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
 RL J. Virol. 68:597-610(1994).
 RN [21]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 94202284.
 RA SCHIEWE U., NEIPEL F., SCHREINER D., FLECKENSTEIN B.;
 RT "Structure and transcription of an immediate-early region in the human
 RL J. Virol. 68:2978-2985(1994).
 RN [23]
 RP SEQUENCE FROM N.A.
 RC STRAIN-U1102, VARIANT A;
 RX MEDLINE; 94181269.
 RA THOMPSON J., CHOUDHURY S., KASHANCHI F., DONIGER J., BERENMAN Z.,
 RT "A transforming fragment within the direct repeat region of human
 Query Match 4.18; Score 7; DB 12; Length 87;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 PRTPPS 103
 DB 4 PRTPPS 10
 RESULT 13
 Q9WT40 PRELIMINARY; PRT; 88 AA.
 ID Q9WT40;
 AC Q9WT40;
 DT 01-NOV-1999 (TRENBLER, 12, Created)
 DT 01-NOV-1999 (TRENBLER, 12, Last sequence update)
 DT 01-NOV-1999 (TRENBLER, 12, Last annotation update)
 DE U24 PROTEIN.
 GN U24.
 OS Human herpesvirus 6.
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Betaherpesvirinae; Roseolovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HST;
 RA ISGAWA Y., MUKAI T., NAKANO K., KAGAWA M., CHEN J., MORI Y.,
 RA SUWAGAWA T., SASHIHARA J., ZOU P., KOSUGE H., YAMAMOTO K.;
 RT "A comparison of the complete DNA sequences between human herpesvirus-

RT 6 variant A and B."
 RL J. Virol. 0:0-0(1999).
 DR EMBL: AB021506; BAA78245.1; -
 SQ SEQUENCE 88 AA; 10237 MW; 44DFB4BE CRC32;

Query Match
 Best Local Similarity 4.1%; Score 7; DB 12; Length 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 PRTPPS 103
 Db 4 PRTPPS 10

RESULT 14
 ID 069048 PRELIMINARY; PRT; 93 AA.
 AC 069048;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE HERPESVIRUS 6 IMMEDIATE-EARLY GENE HOMOLOGUES.
 GN EOLF1.
 OS Human herpesvirus 6.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roseolovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-01102;
 RX MEDLINE: 94118404.
 RA NICHOLAS J., MARTIN M.;
 RT "Nucleotide sequence analysis of a 38.5-kilobase-pair region of the
 genome of human herpesvirus 6 encoding human cytomegalovirus
 RT immediate-early gene homologs and transactivating functions.";
 RL J. Virol. 68:597-610(1994).
 DR EMBL: L25528; AAA16731.1; -
 SQ SEQUENCE 93 AA; 10834 MW; BD463ABE CRC32;

Query Match
 Best Local Similarity 4.1%; Score 7; DB 12; Length 93;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 97 PRTPPS 103
 Db 10 PRTPPS 16

RESULT 15
 ID 031793 PRELIMINARY; PRT; 123 AA.
 AC 031793;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE YMA6. PROTEIN.
 GN YMA6.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE: 98044033.
 RA KUNST F., OGASAWARA N., MOSZER I., ALBERTINI A.M., ALLONI G.,
 RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOTIN A., BORCHERT S.,
 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNETT S.C., BRON S.,
 RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 RA DENISOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
 RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOUDGER D.,
 RA FRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZZI A., GALLERON N.,

RA GHIM S.Y., GLASER P., GOFFENAU A., GOLIGHTLY E.J., GRANDI G.,
 RA GUSEPPT G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A.,
 RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
 RA JORIS B., KARAMATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
 RA KOBAYASHI Y., KOETTER P., KONIGSTEIN G., KROGH S., KUMANO M.,
 RA KURITA K., LAPIDUS A., LARDINOIS S., LAUDER J., LAFARVIC V.,
 RA LEE S.M., LEVINE A., LIT H., NASUDA S., MAUEL C., MEDIGUE C.,
 RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 RA NOONE D., O'REILLY M., OGAWA K., OGIMARA A., OUDEGA B., PARK S.H.,
 RA PARRO V., POHL T.M., PORTELELLA D., POROLOTIK S., PRESCOTT A.M.,
 RA PRESECAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
 RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADATE Y.,
 RA SATO T., SCANTAN E., SCHLEICH S., SCHROETER R., SCORFONE F.,
 RA SEKIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDO B.,
 RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKENARI K.,
 RA TAKEUCHI M., TAKAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
 RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
 RA VIARI A., WAMUTT R., WEDLER E., WEDLER H., WEITZEGGER T.,
 RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUNOTO K., YATA K.,
 RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.,
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Z99113; CAB13615.1; -
 SQ SEQUENCE 123 AA; 13781 MW; C48C6BF8 CRC32;

Query Match
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 Db 71 RPFGRG 77

Search completed: September 26, 2000, 19:38:37
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ACCESSION AL037973
VERSION AL037973.1 GI:5407285
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 526)
AUTHORS Bloecker,H., Beecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE EST (Bloecker, et al.)
JOURNAL Unpublished (1999)
COMMENT On Oct 6, 1998 this sequence version replaced gi:3705332.
Contact: Bloecker H
MIPS
Am Kioferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZ564P227) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
location/Qualifiers
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34 rGAspThrGlyIleLeuAspSerTieGlyArgPhePheGlyLysArg 50
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117 pGlyAlaGluGlyGlnArgProGlyPheGlyTyrGlyArgAlaSerA 134
412 GGGGCGCGAAGGCCAGACACAGATTTGGCTACGGAGCGAGGCGTCCG 461
134 spTyrLysSerAlaHisLysGlyPheLysGlyValAlaPalaGlnGlyThr 150
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5', mRNA sequence.
ACCESSION AU079802
VERSION AU079802.1 GI:6084557
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 808)
AUTHORS Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M.,
Suzuki,Y., Sasaki,M. and Sugano,S.
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DEFINITION AU067431 SUGANO mouse brain mncb Mus musculus cDNA clone MNCB-3446
5', mRNA sequence.
ACCESSION AU067431
VERSION AU067431
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 720)
Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
Unpublished (1999)
On Oct 8, 1998 this sequence version replaced gi:372975.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
2-5-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashishn@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
location/Qualifiers
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organism="Mus musculus"
strain="C57BL/
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clone="MNCB-3446"
FEATURES
source

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 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 779)
 Sasaki,Z., Suzuki,Y., Watanabe,M., Imai,J., Shibui,A., Yoshida,K.,
 Hata,H., Yamaguchi,K., Tateyama,S. and Sugano,S.
 Unpublished (1998)
 TITLE Contact: Katsuyuki Hashimoto
 JOURNAL Division of Genetic Resources
 COMMENT National Institute of Infectious Diseases
 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 Email: khashi@nii.go.jp.
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 ligated to a DraIII adaptor [TGTGGCTACG] / digested
 and cloned into distinct DraIII sites of the pME185-Fl3.
 XhoI sites just outside the DraIII sites can be used to
 isolate the cDNA insert. Size selection was performed to
 exclude fragments <1.5 kb. Library was constructed by

Sugano et al. (University of Tokyo, Institute of Medical
 Science). Custom primer for sequencing: 5' end primer
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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REFERENCE      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS        1 (bases 1 to 804)
TITLE          Sasaki,M., Suzuki,Y., Watanabe,M., Imai,J., Shibus,A., Yoshida,K.,...
JOURNAL        Hata,H., Yamaguchi,R., Tateyama,S. and Sugano,S.
COMMENT        Construction of mouse full length-enriched cDNA libraries by
                oligo-capping
                Unpublished (1999)
                On Jun 5, 1998 this sequence version replaced gi:187684.
                Contact: Katsuyuki Hashimoto
                Division of Genetic Resources
                National Institute of Infectious Diseases
                2-3-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
                Email: khashi@nih.go.jp
                URL: http://www.nih.go.jp/yoken/genbank/
                Seq primer: 5' end primer: CTCTGCTCTAAAGCTGCg.
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               and cloned into distinct DraIII sites of the pME18S-FU3.
               XhoI sites just outside the DraIII sites can be used to
               isolate the cDNA insert. Size selection was performed to
               exclude fragments <1.5 kb. Library was constructed by
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seq_documentation_block:
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VERSION      AU066815
KEYWORDS     AU066815 GI:4967552
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ORGANISM     Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus; 1 (phases 1 to 771)
Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M., Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method
Unpublished (1999)
On Apr 7, 1998 this sequence version replaced gi:3036368.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
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seq_documentation_block:
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DEFINITION AU080522 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-5756
5', mRNA sequence.
ACCESSION AU080522
VERSION AU080522.1 GI:6085276
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 782)
Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M.,
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5408331.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
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[ATGTGGCTTTTCTTTTCTTTT] double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCTCTGCG], digested
and cloned into distinct DraIII sites of the pME18S-FL3.
XhoI sites just outside the DraIII sites can be used to
isolate the cDNA insert. Size selection was performed by
exclude fragments <1.5 kb. Library was constructed by
Sugano et al. (University of Tokyo, Institute of Medical
Science). Custom primer for sequencing: 5' end primer
[CTTCGCTCTAAAGCTGCG]"

BASE COUNT 205 a 213 c 205 g 154 t 5 others
ORIGIN

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533 ATGAAACCCAGTAGTCTCATTTCTTCAAGAACATTTGACACCTCGAAC 582
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100 ProProProSerGlnGlyLysArgGlyLysSerLeuSerLeuArgPheSe 116
|||||
583 CCACCTCATCTCCAGAGGAGGAGGAGGCTGTCCCTCAGCAGATTAG 632
|||||
116 TTPGlyAlaGlyLysGlnArgProGlyPheGlyTyrGlyArgAlaAs 133
|||||
633 CTGGGGGCGGAGGCGCAGAACGACGATTTGGCTACNGAGCAGAGCTT 682
|||||
133 eRAspTyrLysSerAlaHisLysGlyPheLysGlyVal...AspAlaGln 148
|||||
683 NCGACTATTAATCGNTCAGACAGGATTCAAGGGGCGCTCAGCGCCAG 722
|||||
149 GYTHrLeuSerLysIlePheLysLeuGlyLysArgAspSerArg 164
|||||
733 GGCACGCTTTCMAATCTTAACTGGAAGAAAGAACACCGGNTCT 780

seq_name: gb_est29:AU066924

seq_documentation_block:
LOCUS AU066924 770 bp mRNA EST 02-JUN-1999
DEFINITION AU066924 Sugano mouse brain mncb Mus musculus cDNA clone MNCB-2726
5', mRNA sequence.
ACCESSION AU066924
VERSION AU066924.1 GI:4967661
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 770)
Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A., Hirata, M.,
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brain cDNA
library made by oligo-capping method
Unpublished (1999)
On Apr 7, 1998 this sequence version replaced gi:3036477.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
1..770
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="MNCB-2726"
/clone_lib="Sugano mouse brain mncb"
/sex="female"
/dev_stage="adult"
/lab_host="TOP10"
/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTCTTTTCTTTT] double-stranded cDNA was

```

ligated to a DraIII adaptor (TGTGGCCTACTGG), digested and cloned into distinct DraIII sites of the pHE188-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer for sequencing: 5' end primer [CTTCTCTCTTAAAGTCTGG]

BASE COUNT 184 a 225 c 201 g 151 t 9 others
ORIGIN

alignment_scores:
Quality: 750.50 Length: 173
Ratio: 4.811 Gaps: 5
Percent Similarity: 90.173 Percent Identity: 86.705

alignment_block:
US-09-218-277-12 x AU066924 ..

Align seg 1/1 to: AU066924 from: 1 to: 770

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1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
|||||
48 ATGGCATCACAAGAGACCTCCACAGCA.....TCCAGTACTGGC 91
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
92 CACAGCAGTACCATGACATGACATGACGATGCTCTCCCAAGCACA 141
|||||
34 rGAspThrGlyLeuAspSerLysGlyArgPhePheGlyLysAspArg 50
|||||
142 GAGAACGGGCACTCTGACTCCATCGGGCGCTTTTGCGGTGACAG 191
|||||
51 GAlaLProLysArgLysSerGlyLysAspSerHisProAlaArgTh 67
|||||
192 GGTGGCCCAACGGGGCTCTGCAAGACTCAC.....ACGAGAAC 235
|||||
67 rAlaHisTyrGlySerLeuProGlnLysSer...HisGlyArgThrGln 83
|||||
236 TACCCTATATGGCTCCCTCCCAAGATCGACGACGCGGACCAAG 285
|||||
83 sPGLAsnProValAlaHisPhePheLysAsnLLeValThrProArgThr 99
|||||
286 ATGAAACCCAGTACATCTCTTCAAGACATGTGTGACACCTCGAACA 335
|||||
100 ProProSerSerGlnLysGlyArgGlyLeuSerLeuSerArgPheSe 116
|||||
336 CCACCTCCATCCCAAGGAG..... 356
|||||
116 rTrpGlyAlaGlnLysGlnArgProGlyPheGlyTyrGlyArgAlas 133
|||||
357 ...GGGGCCGAGGGGACAGACGAGATTGCTACGAGAGAGCTT 402
|||||
133 eAspTyrLysSerAlaHisLysGlyPheLysGlyAla...AspAlaGln 148
|||||
403 CGACATATAATCGGCTCACAGGAGATTCAAGGGGCTCACGCGCCAG 452
|||||
149 GAlThrLeuSerLysLLePheLysLeuGlyLysArgAspSerArgSer 165
|||||
453 GGCACGCTTCCAAAATCTTTAAGCTGGAGAGAGACAGCCGCTCTGG 502
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165 ySerProMetAlaArgArg 171
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503 ATCTCCCATGGGAGAGCG 521
|||||
seq_name: gb_est6:AA352612
seq_documentation_block:
LOCUS AA352612 511 bp mRNA EST 21-Apr-1997
DEFINITION EST60632 Activated T-cells xx Homo sapiens cDNA 5' end similar to
myelin basic protein, mRNA sequence.
ACCESSION AA352612

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VERSION AA352612.1 GI:2004932
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 511)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A.,
Bull,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'wal,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitchum,W.M., Fritchman,J.L., Geoghagen,N.S.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,D.M.,
Moreno-Palacios,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utebback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrite,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,R.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
JOURNAL MEDLINE
COMMENT Other ESTs: THC171045
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES
source
location/Qualifiers
1..511
/organism="Homo sapiens"
/db_xref="ATCC (inhost):152811"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 124 a 141 c 145 g 89 t 12 others
ORIGIN

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alignment_scores:
Quality: 749.00 Length: 160
Ratio: 4.993 Gaps: 2
Percent Similarity: 93.750 Percent Identity: 89.375

alignment_block:
US-09-218-277-12 x AA352612 ..

Align seg 1/1 to: AA352612 from: 1 to: 511

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1 MetAlaSerGlnLysArgProSerGlnArgHisGlySerLysTyrLeuAl 17
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36 ATGGCATCACAAGAGACCTCCACAGCAAGGATCCCAAGTACTGGC 85
|||||
17 aThrAlaSerThrMetAspHisAlaArgHisGlyPheLeuProArgHisA 34
|||||
86 CACAGCAGTACCATGACATGACATGACGATGCTCTCCCAAGCACA 135
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34 rGAspThrGlyLeuAspSerLysGlyArgPhePheGlyLysAspArg 50
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```

```
|||||  
136 GAGACAGGGCATCNTGACTCCATCGGGCGCTTCTTGCGGGTGAACG 185  
51 GlyAlaProLysArgGlySerGlyLysAspSerHisProAlaArgTh 67  
|||||  
186 GGTCCGCGCTAATCGGGGCTCTGGCAAGACTNACACCACCGGCAAGAAC 235  
67 rAlaHisTyrGlySerLeuProGlnLysSerHisGlyArgThrGlnAspG 84  
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236 TGCCTACTATGGCTCCTGCTGCCAGAGTCACAGGGCGGAGCCAAAGATG 285  
84 LysnProValValHisPhePheLysAsnIleValThrProArgThrPro 100  
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286 AAACCCCGTAGTCACACTTCTCAAGAACATNTNAGCCCTNGACACACA 335  
101 ProProSerGlnGlyLysGlyArgGlyLeuSerLeuSerArgPheSerTr 117  
|||||  
336 CCCCCTGNCAGGGAAAGGGAGAGACTGCTCCCTGAGCAGATTAGCTG 385  
117 pGlyAlaGlnGlyGlnArgProGlyPheGlyTyrGlyArgAlaSerA 134  
|||||  
386 GGGGGCCGAANAGTAGNACCAGGATTTGGCTACGGAGGAGCGGTCCG 435  
134 sPTyrLysSerAlaHisLysGlyPheLysGlyValAspAlaGlnGlyTh 150  
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436 ACTATAATCGGNTCACAGGNTTCAAGGAGTTCATGNCACAGGAGNAC 485  
150 rLeuSerLysIlePheLysLeuGly 158  
|:::|||||  
486 GTTTTCAAAAATTTTAAGTTGGG 511
```


KW experimental allergic encephalomyelitis; EAE; analogue.
OS Homo sapiens.
PN MO9616086-A1.
PD 30-MAY-1996.
PF 16-NOV-1995; U14403.
PR 18-NOV-1994; US-342408.
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.
PI Conlon PJ, Gaur A, Ling N, Steinman L;
DR MPI; 96-268535/27.
DR N-PSDB; T32561.
PT Peptide analogues of human myelin basic protein - useful for treatment of multiple sclerosis
PS Disclosure: Figure 1; 61pp; English.
CC Peptide analogues comprising at least seven amino acids from residues 86-99 of human myelin basic protein (MBP), can be used to treat multiple sclerosis by competing for the binding of native MBP
CC Peptide to MHC and by not causing proliferation of an MBP reactive T-cell line. The peptide analogues also inhibit the induction of experimental allergic encephalomyelitis (EAE) by MBP in rodents.
CC The peptide analogues have a reduced susceptibility to proteolysis in vivo.
CC Sequence 171 AA;

Query Match 100.0%; Score 922; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 3.1e-90;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASOKRPSORHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFGDGDGAPRSGSKD 60
D 1 MASOKRPSORHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFGDGDGAPRSGSKD 60
QY 61 SHHPARTAHYGSLEPQKSHGRTODENPVHFEKNIIVTPRTPPPSGKRGSLSRFSWGA 120
D 61 SHHPARTAHYGSLEPQKSHGRTODENPVHFEKNIIVTPRTPPPSGKRGSLSRFSWGA 120
QY 121 GQRFEGYGRASDYKSAHKGFGVDAGQGLSKIFKLGSDSRSGSPMAR 171
D 121 GQRFEGYGRASDYKSAHKGFGVDAGQGLSKIFKLGSDSRSGSPMAR 171

RESULT 3
R48592
ID R48592 standard; protein; 170 AA.
AC R48592;
DE 31-JUL-1994 (first entry)
KW Human myelin basic protein.
KM Protolipid protein; myelin basic protein; retrovirus;
KW neurodegenerative disease; by-stander antigen; TGF-beta;
KW transforming growth factor-beta; T-cell; T-lymphocyte;
KW myelopathy; paraparesis; human immunodeficiency virus type 1.
OS Homo sapiens.
PN MO9404121-A.
PD 03-MAR-1994.
PF 17-AUG-1993; U07786.
PR 17-AUG-1992; US-931217.
PA (AUTO-) AUTOIMMUNE INC.
PI Hafner DA, Weiner HL;
DR MPI; 94-082786/10.
PT Treating retroviral associated neurological disease - by admin. of by-stander antigen, causing release of transforming growth factor beta from suppressor T cells
PS Disclosure: Page 49; 64pp; English.
CC Myelin basic proteins (sequences R48592-96) and cattle proteolipid protein (R48592) elicit the release of TGF-beta from suppressor T-cells and target the T-cells to neural tissue under cytotoxic attack, thereby reducing neurological disease, e.g. HIV-1
CC associated myelopathy, tropical spastic paraparesis and HIV infection.
CC Sequence 170 AA;

Query Match 99.5%; Score 917; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 1e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFGDGDGAPRSGSKD 61
D 1 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFGDGDGAPRSGSKD 60
QY 62 HHBPARTAHYGSLEPQKSHGRTODENPVHFEKNIIVTPRTPPPSGKRGSLSRFSWGA 121
D 62 HHBPARTAHYGSLEPQKSHGRTODENPVHFEKNIIVTPRTPPPSGKRGSLSRFSWGA 120
QY 122 GQRFEGYGRASDYKSAHKGFGVDAGQGLSKIFKLGSDSRSGSPMAR 171
D 121 GQRFEGYGRASDYKSAHKGFGVDAGQGLSKIFKLGSDSRSGSPMAR 170

RESULT 4
R95406
ID R95406 standard; protein; 170 AA.
AC R95406;
DE 16-DEC-1996 (first entry)
KW Myelin oligodendrocyte protein.
KM Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE;
KW CD4+ T-cell; autoimmune disease; demyelination; central nervous system;
KW CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG;
KW relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP;
KW diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
KW psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
KW myelin oligodendrocyte protein; myelin associated glycoprotein; therapy.
OS Homo sapiens.
PN MO9612737-A2.
PD 02-MAY-1996.
PR 25-OCT-1995; U13682.
PR 25-OCT-1994; US-328224.
PR 15-MAR-1995; US-404228.
PR 25-OCT-1995; ZA-009033.
PA (IMMU-) IMMUNOLOGIC PHARM CORP.
PI Devaux B, Franzen R, Geller M, Hsu D, Pallard X;
PI Rothbard J, Samson M, Shi J, Smlek D;
DR MPI; 96-230552/23.
PT Myelin basic derived peptide(s) and analogs - used in the treatment of Multiple Sclerosis, psoriasis, Graves Disease, etc.
PS Example 9; Fig 1; 91pp; English.
CC This sequence represents the human myelin oligodendrocyte protein (MOG).
CC Immunisation with MOG (or the peptide fragments shown in R95375-R95385)
CC can be used to induce experimental allergic encephalomyelitis (EAE) in
CC susceptible strains of mice. EAE is a CD4+ T-cell mediated autoimmune
CC disease which results in demyelination of the central nervous system,
CC resulting in paralysis and other neurological abnormalities. EAE is a
CC commonly used animal model for human multiple sclerosis (MS). These
CC sequences can be used in compositions for treating MS in a mammal. The
CC composition acts to down regulate the autoimmune response, and may be
CC administered in an amount sufficient to prevent the onset of symptoms of
CC MS. The compositions may also be used to treat advanced stage MS,
CC especially relapsing-remitting MS, chronic progressive MS or benign MS.
CC These peptides may also be used in the treatment of other diseases
CC involving myelin autoantigens, including diabetes, Graves disease,
CC myasthenia gravis, Good Pasture's syndrome, psoriasis, thyroiditis, and
CC rheumatoid arthritis. Peptides derived from other myelin autoantigens,
CC such as myelin basic protein (MBP, see R95334-R95374), proteolipid
CC protein (PLP), and myelin associated glycoprotein (MAG) can be used as
CC alternatives to the MOG peptides in these compositions.
CC Sequence 170 AA;

Query Match 99.5%; Score 917; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 1e-89;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFGDGDGAPRSGSKD 61
D 1 ASOKRPSORHGSKYLTASTMDHARHGFLPRHRDTGILDSIGRFGDGDGAPRSGSKD 60

QY 62 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGRGSLSTSFSGAG 121
 DB 61 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGRGSLSTSFSGAG 120
 QY 122 QRRGFGYGRASDYKSAHKFGKVDAGTSLSTFKLGDRSRSRSGPMARR 171
 DB 121 QRRGFGYGRASDYKSAHKFGKVDAGTSLSTFKLGDRSRSRSGPMARR 170

RESULT 5
 R35440
 ID R35440 standard; protein: 170 AA.
 AC R35440-1993 (first entry)
 DT 13-AUG-1993
 DE Human basic myelin protein.
 KM BMP; MS; multiple sclerosis; homologue; myelin basic protein; MBP.
 OS Homo sapiens.
 FH Key
 FT peptide Location/Qualifiers
 FT 61..106
 FT /note= "neutralising fragment"
 FT 1..15
 FT /note= "neutralising fragment"
 FT 4..18
 FT /note= "neutralising fragment"
 FT 9..23
 FT /note= "neutralising fragment"
 FT 15..35
 FT /note= "neutralising fragment"
 FT 20..37
 FT /note= "neutralising fragment"
 FT 31..46
 FT /note= "neutralising fragment"
 FT modified_site
 FT 1
 FT /note= "acylated"
 PN W09308212-A.
 PD 29-APR-1993.
 PF 15-OCT-1992; CA0448.
 PR 22-OCT-1991; CA-053799.
 PA (CATZ/) CATZ I.
 PA (MARR/) WARREN K G.
 PI Catz I. Warren KG;
 WPI 93-152422/18.
 DR Homologous peptide analogues of human basic myelin protein - used
 PT for treating multiple sclerosis
 PS Disclosure: Fig 4; 26pp; English.
 CC The sequence is that of human basic myelin protein (BMP). Fragments
 CC of this sequence are claimed (see features) which are able to
 CC neutralise anti-BMP antibodies and are thus useful in treatment of
 CC multiple sclerosis. The fragments may be prepd. synthetically and
 CC avoids the dangers associated with the use of the natural protein,
 CC e.g. transmission of neuroviruses. Also the peptides are too small
 CC to be immunogenic.
 SQ Sequence 170 AA.

Query Match 98.6%; Score 909; DB 1; Length 170;
 Best Local Similarity 98.8%; Pred. No. 7.4e-89;
 Matches 168; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 ASQKRPSQHRGSKYLATASTMDHARHGLPRHRDTGILDSIGRFGGDRGAPRKSGKDS 61
 DB 1 ASQKRPSQHRGSKYLATASTMDHARHGLPRHRDTGILDSIGRFGGDRGAPRKSGKDS 60
 QY 62 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGRGSLSTSFSGAG 121
 DB 61 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNIVTPRTPPPSQGRGSLSTSFSGAG 120
 QY 122 QRRGFGYGRASDYKSAHKFGKVDAGTSLSTFKLGDRSRSRSGPMARR 171
 DB 121 QRRGFGYGRASDYKSAHKFGKVDAGTSLSTFKLGDRSRSRSGPMARR 170

RESULT 6

W00399
 ID W00399 standard; protein: 197 AA.
 AC W00399;
 DT 01-FEB-1997 (first entry)
 DE Human myelin basic protein (foetal isoform).
 KM Myelin basic protein; MBP; MBP+X2Cys81; proteolipid protein; PLP;
 KM Multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KM T-lymphocyte; T-cell; anergy; apoptosis.
 OS Homo sapiens.
 FH Key
 FT region Location/Qualifiers
 FT 60..85
 FT /label= X2
 FT /note= "exon 2-encoded region"
 FT misc_difference 81
 FT /note= "Cys-81 may be replaced by any standard
 FT amino acid, esp. an uncharged amino acid
 FT of mol.wt. below about 150, partic.
 FT Ser, in constructs of the invention"

W09634622-A1.
 PD 07-NOV-1996.
 PE 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo Mj, Mattis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI 96-505898/50.
 DR N-PSDB; T41889.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Claim 1: Page 79-80; 156pp; English.
 CC The native human 21.5 kDa foetal isoform (W00399) of myelin basic
 CC protein, MBP+X2Cys81, includes an exon 2-encoded region (X2) that
 CC may contain an epitope involved in the pathogenesis of multiple
 CC sclerosis (MS); the X2 region is not found in the MBP of healthy
 CC adults. Recombinant MBP+X2, or variants modified to improve
 CC bacterial expression (see also W06107), can be produced in a
 CC large scale in bacterial hosts. They are useful for assaying
 CC T-cells for responsiveness to MBP epitopes and can be used as
 CC therapeutic agents that act by inducing T-cell responses,
 CC including anergy and apoptosis, as a means of treating MS.
 SQ Sequence 197 AA;

Query Match 97.5%; Score 899; DB 1; Length 197;
 Best Local Similarity 86.8%; Pred. No. 1e-87;
 Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MASQKRPSQHRGSKYLATASTMDHARHGLPRHRDTGILDSIGRFGGDRGAPRKSGV 58
 DB 1 MASQKRPSQHRGSKYLATASTMDHARHGLPRHRDTGILDSIGRFGGDRGAPRKSGV 60
 QY 59 -----KDSHHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNI 94
 DB 61 PWLKGSRSLPSPHANSQPELCMYKDSHHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNI 120
 QY 95 VTPRTPPPSQGRGSLSTSFSGAGRGORPGFGYGRASDYKSAHKFGKVDAGTSLST 154
 DB 121 VTPRTPPPSQGRGSLSTSFSGAGRGORPGFGYGRASDYKSAHKFGKVDAGTSLST 180
 QY 155 FRLGDRSRSRSGPMARR 171
 DB 181 FRLGDRSRSRSGPMARR 197

RESULT 7
 W06107
 ID W06107 standard; protein: 203 AA.
 AC W06107;
 DT 01-FEB-1997 (first entry)

	Foetal myelin basic protein MBP+X2Cys81/Bact.
KM	Myelin basic protein; MBP; MBP-x2cys81; proteolipid protein; PLP;
KW	multiple sclerosis; autoimmune disease; diagnosis; therapy;
OS	T-lymphocyte; T-cell; energy; apoptosis.
FH	Synthetic.
FT	Key
FT	region
FN	Location/Qualifiers
PD	60..85
PT	/label= X2
PF	/note= "exon 2-encoded region"
PZ	
PR	M09634622-A1.
PA	07-NOV-1996.
PI	22-APR-1996; U05611.
PP	02-MAY-1995; US-431648.
PR	02-MAY-1995; US-431644.
PR	07-JUN-1995; US-482114.
PA	(ALEX-) ALEXION PHARM INC.
PA	(USSR) US DEPT HEALTH & HUMAN SERVICES.
PI	Lennardo MJ, Matlis L, McFarland HF, Mueller EE, Mueller JP;
PI	Nye SH, Pelfrey CM, Squinto SP, Wilkins JI.
DR	MBP: 96-505898/50.
DR	N-PDSB; T41896.
PT	New human myelin basic protein and proteolipid protein variant(s) -
PT	used in the assessment, diagnosis and treatment of multiple
PT	sclerosis
PS	disclosure: Page 81-82; 156pp; English.
CC	A 21.5 kDa foetal isoform (W06107) of myelin basic protein,
CC	MBP+x2Cys81/bact., is the product of a DNA construct (T41896)
CC	based on the human foetal MBP+x2Cys81 isoform (W00399) but
CC	utilising bacterially-preferred codons in place of the native human
CC	codons (see also T41889). This increases prodn. of the MBP in E.
CC	coli by at least 50%. Recombinant MBP 21.5 polypeptides (see also
CC	W00399 and W06108) are useful in the clinical assessmt, diagnosis
CC	and treatment of MS.
Q	Sequence 203 AA:

Query Match	97.5%;	Score 899;	DB 1;	length 203;
Best Local Similarity	86.8%;	Pred. No. 1e-87;		
Matches 171; Conservative	0;	Mismatches	26;	Gaps 1;

QY	1	MASQRRPSQRHGSKYLLATASTMDHARGLPLRHDDTILDSIGRFFGGDGAAPKRGSG--	58
Db	1	MASQRRPSQRHGSKYLLATASTMDHARGLPLRHDDTILDSIGRFFGGDGAAPKRGSGKV	60
QY	59	-----KDSHPAPRTAHYGSLEPQSKSHGTQDENPVVHEFFKNT	94
Db	61	PWLKPGRSPLPSHARSGPGLCNMTKDSHHPARTAHYGSLSPQSKSHGTQDENPVVHEFFKNT	120
QY	95	VTPRTPPPSQGGKGRGLSLRFSWMAEGORPGFGYGRASDYKSKHKGFKGVDAQGTLSKI	154
Db	121	VTPRTPPPSQGGKGRGLSLRFSWMAEGORPGFGYGRASDYKSKHKGFKGVDAQGTLSKI	180
QY	155	FKLGGDRSRSGSPMARR 171	
Db	181	FKLGGDRSRSGSPMARR 197	
RESULT	8		
W06108			
ID	W06108	standard; Protein; 203 AA.	
AC	W06108;		
DT	01-FEB-1997	(first entry)	
DE	Foetal myelin basic protein MBP-x2Ser81/bact.		
KM	Myelin basic protein; MBP; MBP-x2Ser81; proteolipid protein; PLP;		
KM	multiple sclerosis; autoimmune disease; diagnosis; therapy;		
KW	T-lymphocyte; T-cell; anergy; apoptosis.		
OS	Synthetic.		
FH	Key		
FT	region	location/Qualifiers	
FT		60..85	
FT		/label=x2	
FT		/note="exon 2-encoded region, with Cys81Ser	
FT		mutation"	
FT	peptide	196..203	

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FT /label= Hexa-histidine tag  
FT /note= "the hexa-histidine tag facilitates  
FT purification of the recombinant protein  
FT from host cells"  
FN WO9634622-A1.
```

PN WO/9634622-A1.
PF 07-NOV-1996.
PF 22-APR-1996; 005611.
PR 02-MAY-1995; US-431648.
PR 02-MAY-1995; US-431644.
PR 07-JUN-1995; US-482114.
PA (ALEX-) ALEXION PHARM INC.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI Leonardo MJ, Mattis L, McFarland HF, Mueller EE, Mueller JP;
PI Nye SH, Pelletier CM, Squinto SP, Wilkins JA;
DR WPI; 96-503898/50.
DR N-PSDB; T41897.
PT New human myelin basic protein and proteolipid protein variant(s) -
PT used in the assessment, diagnosis and treatment of multiple
PT sclerosis
PS Disclosure; Page 82-83; 156pp; English.
PS A 21.5 kDa foetal isoform (W06108) of myelin basic protein,
CC MBP+XSe81/Dact., is the product of a DNA construct (T41897)
CC based on the human foetal MBP+X2Cys81 isoform (W00399) but
CC utilizing codons that are highly expressed in bacterial genes in
CC place of the native codons (see also T41889) and incorporating a
CC sequence coding for a hexa-histidine tail. This allows large-
CC scale prodn. and purification of the MBP in bacterial hosts
CC Recombinant MBP 21.5 polypeptides (see also W00399 and W06107) are
CC useful in the clinical assessment, diagnosis and treatment of MS.
SQ Sequence 203 AA;

Query Match	97.58;	Score 899;	DB 1;	Length 203;
Best Local Similarity	86.88;	Pred. No. 1e-87;		
Matches 171; Conservative	0;	Mismatches	0;	Indels 26; Gaps 1

```
QY      1 MASGRPSQRHGSKYLATASTMDHARHGFLPRHRDGLDSIGRFEGGDRGAPKRSG--   58
        |||||
DB       1 MASGRPSQRHGSKYLATASTMHARHGFLPRHRDGLDSIGRFFGGDRGAPKRGSKV   60
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QY	59	-----	KDSHPAPTAHYGLSPQKSHGRTPQDENPVVHEFFKNI	94
Db	61	PWLKPGKSPLEPSHAHRSQPGLSNMTKDSHHHARRAHYSLPQKSHGRTPQDENPVVHEFFKNI	120	
QY	95	VTPRTPPPSQCKGKGLSLSRFSWGAEGQRPFGYGYGRASDYKSAHKKGFKGVDAQGLTSKI	154	
Db	121	VTPTPTPPPSQCKGKGLSLSRFSWGAEGQRPFGYGYGRASDYKSAHKKGFKGVDAQGLTSKI	180	
QY	155	FKLGRDSRSGSPMARR	171	
Db	181	FKLGRDSRSGSPMARR	197	
RESULT	9			
W06103				
ID	W06103	standard; Protein; 373 AA.		
AC	01-FEB-1997	(first entry)		
DE	MP4 chimera (MBP21.5-delta P1P4 fusion).			
KW	Proteolipid protein; P1P; delta P1P3; myelin basic protein; MBP;			
KW	MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;			
KW	therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.			
OS	Synthetic.			
FH	Key	Location/Qualifiers		
FT	protein	1..368		
FT	domain	/note="preferred protein of the invention"		
FT	peptide	1..197		
FT	peptide	/label= MBP21.5		
FT	domain	198..200		
FT	domain	/label= Spacer		
FT	peptide	201..373		
FT	peptide	/label= Delta_P1P4		
FT	peptide	201..205		

FT	/note= "synthetic N-terminal peptide not found in
FT	the native protein"
FT	208..219
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	210..230
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	241..261
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	242..259
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	244..257
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	248..269
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	256..269
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	257..269
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	268..281
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	270..303
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	292..304
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	292..307
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	293..306
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	314..326
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	326..337
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	326..339
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	351..365
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	213..234
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	292..304
FT	/label= Epitope
FT	/note= "PVP epitope associated with MS"
FT	369..373
FT	/label= Hisidine tag
FT	/note= "hexa-histidine tag facilitates recombinant
FT	protein purification"
FT	W09634622-A1.
PD	07-NOV-1996.
PD	22-APR-1996; U05611.
PR	02-MAY-1995; US-431648.
PR	02-MAY-1995; US-431644.
PR	07-JUN-1995; US-482114.
PA	(ALEX-) ALEXION PHARM INC.

Query	Subject	Accession	Score	Length	Gap
QY	1	MASQKRPQSRHSGKYATASTMDHARHGF.LPRHRDTGLDLSIGREFFGDRGAPKRGSG--	97.5%;	373;	
Db	1	MASQKRPQSRHSGKYATASTMDHARHGF.LPRHRDTGLDLSIGREFFGDRGAPKRGSGKV	Best Local Similarity 86.8%;	Pred. No. 2,2e-87;	
QY	59	-----KSHHPARTAHGSL.PQKSHRGRTQDENPVYHFFNNI	Matches 172; Conservative 0; Mismatches 0; Indels 26; Gaps		
Db	61	PWLKPGSSPLPSHARSQPGICNNYKQSHHPARTAHAGSL.PQKSHRGRTQDENPVYHFFNNI			
QY	95	VTPPTPPSQGKGRGLSLSPFSWGAEQGPFGFGYGGGRASDYSAKHGFGVDAQGTLSKI			
Db	121	VTPPTPPSQGKGRGLSLSPFSWGAEQGPFGFGYGGGRASDYSAKHGFGVDAQGTLSKI			
QY	155	FKLGGDRSRSGSPMAR 171			
Db	181	FKLGGDRSRSGSPMAR 197			
RESULT	10				
ID	W06102	W06102 standard; Protein: 385 AA.			
AC	W06102;				
DT	01-FEB-1997	(first entry)			
DE	MP3 chimera (MBP21.5-delta PLP3 fusion).				
KW	Proteolipid protein; PLP; delta PLP3; myelin basic protein; MBP;				
RW	MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;				
KW	therapy; T-lymphocyte; T-cell; anergy; apoptosis; MP3 chimera.				
OS	Synthetic.				
EH	key	Location/Qualifiers			
FT	domain	1..197			
FT	peptide	/label= MBP21.5			
FT	peptide	198..200			
FT	domain	/label= Spacer			
FT	domain	201..385			
FT	domain	/label= Delta_PLP3			
PN	W09634622-A1.				
PD	07-NOV-1996.				
PF	22-APR-1996; U05611.				
PR	02-MAY-1995; US-431648.				
PR	02-MAY-1995; US-431644.				
PR	07-JUN-1995; US-482114.				
PA	(ALEX-) ALEXION PHARM INC.				
PA	(USSH-) US DEPT HEALTH & HUMAN SERVICES.				
PI	Lenardo MJ, Mattis L, McFarland HF, Mueller EE, Mueller JP;				
PI	Nye SH, Pelletier CM, Squinto SP, Wilkins JA;				
DR	WP1: 96-505898/50.				
DR	N-PSDB: T41893.				
PT	New human myelin basic protein and proteolipid protein variant(s)				
PT	used in the assessment, diagnosis and treatment of multiple				
PT	sclerosis				
PS	Claim 34; Page 110-112; 156pp; English.				
CC	MP3 chimera (W06103) is a fusion protein composed of human myelin				
CC	basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and				
CC	delta PLP4 (W06100), a proteolipid protein (PLP) muten that lacks				
CC	all 4 hydrophobic domains of native human PLP (W06106) but				
CC	includes PLP epitopes associated with multiple sclerosis (MS). It				
CC	can be expressed in E. coli transformants using a DNA construct				
CC	(T41893) contg. the MBP21.5-delta PLP4 gene fusion. MP4 chimera				
CC	and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)				
CC	are useful for the clinical assessment, diagnosis and treatment				
MS	of MS.				
SO	Sequence 373 AA;				

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PT used in the assessment, diagnosis and treatment of multiple
PT scleriosis
PS Claim 33: Page 108-110; 156pp; English.
CC MP3 chimera (W06102) is a fusion protein composed of human myelin
CC basic protein (MBP) foetal isoform MBP21.5 (see also W00399) and
CC delta PLP3 (W00400), a proteolipid protein (PLP) mutain that lacks
CC hydrophobic domains 1, 3 and 4 of native human PLP (W06106) but
CC includes PLP epitopes associated with multiple sclerosis (MS). It
CC can be expressed in E. coli transformants using a DNA construct
CC (T41892) contg. the MBP21.5-delta PLP3 gene fusion. MP3 chimera
CC and other novel PLP/MBP21.5 polypeptides (W00399-400, W06101-08)
CC are useful for the clinical assessment, diagnosis and treatment
CC of MS.
SQ Sequence 385 AA:

Query Match 97.5%; Score 899; DB 1; Length 385;
Best Local Similarity 86.8%; Pred.No. 2.3e-87;
Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

OY 1 MASOKRPSQHGSKYLATASTMDHARGFLPRHRDGIIDSGREFGDRGAPKRGSG-- 58
    |||||||
DB 1 MASOKRPSQHGSKYLATASTMDHARGFLPRHRDGIIDSGREFGDRGAPKRGSGKV 60
OY 59 -----KDSHPARTAHYGSILPQKSHGRTQDENPVHFEKNI 94
    |||||||
DB 61 PWLKGSRPLPSHARSQPLCNMYKDSHHPARTAHGSLPQKSHGRTQDENPVHFEKNI 120
OY 95 VMPPRPPSGGKRGSLSRFSWGAGRGORPGFGYGRASAHKGFQVDAOGTLSKI 154
    |||||||
DB 121 VVPRTPPSGGKRGSLSRFSWGAGRGORPGFGYGRASAHKGFQVDAOGTLSKI 180
OY 155 FKLGDRSRGSGPMARR 171
    |||||||
DB 181 FKLGDRSRGSGPMARR 197

RESULT 11
W06105 W06105 standard; Protein; 492 AA.
AC W06105:
DT 01-FEB-1997 (first entry)
DE MMOGP4 chimera (MBP21.5-MOG-delta PLP4 fusion).
KW Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;
KW MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
KW therapy; T-lymphocyte; T-cell; MMOGP4 chimera;
KW myelin oligodendrocyte glycoprotein; MOG.
OS Synthetic.
FH Key
FT Location/Qualifiers
FT 1..487
FT /note= "preferred protein of the invention"
FT FT domain
FT 1..197
FT /label= MBP21.5
FT FT domain
FT 198..319
FT /label= MOG
FT FT domain
FT /note= "MOG extracellular domain"
FT 320..486
FT /label= Delta_PLP4
FT FT region
FT 327..338
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT 329..349
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT FT region
FT 360..380
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT FT region
FT 361..278
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT FT region
FT 363..376
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT FT region
FT 367..378
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT FT region
FT 375..388
FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT FT region
FT 376..388
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FT /note= "PLP epitope associated with MS"
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FT 387..400
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FT FT region
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FT /label= Epitope
FT /note= "PLP epitope associated with MS"
FT FT region
FT 332..353
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT FT region
FT 375..388
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT FT region
FT 411..423
FT /label= Epitope
FT /note= "encephalitogenic epitope in mouse model"
FT FT peptide
FT 487..492
FT /label= Histidine tag
FT /note= "hexa-histidine tag facilitates recombinant
FT protein purification"
FT FT
FT W09634622-A1.
FT PN 07-NOV-1996.
FT PD 22-APR-1996; U05611.
FT PE 02-MAY-1995; US-431648.
FT PR 02-MAY-1995; US-431644.
FT PR 07-JUN-1995; US-482114.
FT PA (ALEX-) ALEXION PHARM INC.
FT PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
FT PI Leonardo M; Mats L, McFarland HF, Mueller EE, Mueller JP;
FT PI Nye SH, Palfrey CM, Squinto SP, Walkins JA;
FT DR WPI. 96-505898/50.
FT DR N-PEDB; T41893.
FT PT New human myelin basic protein and proteolipid protein variant(s) -
FT used in the assessment, diagnosis and treatment of multiple
FT PT sclerosis
FT PS Claim 36: Page 115-117; 156pp; English.
CC MMOGP4 chimera (W06105) is a fusion protein composed of human myelin
CC basic protein (MBP) foetal isoform MBP21.5 (see also W00399), the
CC extracellular domain of human myelin oligodendrocyte glycoprotein
CC (MOG) and delta PLP4 (W06101), a proteolipid protein (PLP) mutain.
CC MBP21.5, PLP and MOG are all recognised by autoreactive T cells from
CC multiple sclerosis (MS) patients. The chimera was produced using the
CC a DNA construct (T41893) obtd. by inserting a sequence encoding the
CC MOG moiety into MP4 chimera DNA (see also T41893). MMOGP4 chimera

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CC can be expressed in bacterial cell hosts. PLP and MBP polypeptides
 CC (see also W00400, W06101-04, W06107-08) are useful in the clinical
 CC assessment, diagnosis and treatment of MS.
 SQ Sequence 492 AA;

Query Match 97.5%; Score 899; DB 1; Length 492;
 Best Local Similarity 86.8%; Pred. No. 3e-87;
 Matches 171; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

QY 1 MASOKRPSQKRGSKYLAATSTMDHARHGFLLPRHNDTGLDLSIGRFGGDRAKPKRGSG-- 58
 |||||
 Db 1 MASOKRPSQKRGSKYLAATSTMDHARHGFLLPRHNDTGLDLSIGRFGGDRAKPKRGSGSKV 60
 QY 59 -----KDSHHPARTAHYGSLLPKSHQRTODENPVVHFFKNI 94
 |||||
 Db 61 PWLKPGRSPLPSHARSOPGLCNMYKDSHHPARTAHYGSLLPKSHQRTODENPVVHFFKNI 120
 QY 95 VTPTPTPSQKRGSLSTRSGWGAEGORPGFGYGRASDYKSAHKRGKYDAOGTLSKI 154
 |||||
 Db 121 VTPTPTPSQKRGSLSTRSGWGAEGORPGFGYGRASDYKSAHKRGKYDAOGTLSKI 180
 QY 155 FKLGGRDSRSGSPMAR 171
 |||||
 Db 181 FKLGGRDSRSGSPMAR 197

RESULT 12
 W06104
 ID W06104 standard: Protein; 375 AA.
 AC W06104;
 DT 01-FEB-1997 (first entry)
 DE PM4 chimera (delta PLP4-MBP21.5 fusion).
 KM Proteolipid protein; PLP; delta PLP4; myelin basic protein; MBP;
 KM MBP21.5; multiple sclerosis; autoimmune disease; diagnosis;
 KM therapy; T-lymphocyte; T-cell; PM4 chimera.
 OS Synthetic.
 FH Key
 FT Location/Qualifiers
 FT 6..374
 FT /note= "preferred PM4 chimera protein"
 FT domain
 FT 1..169
 FT /label= Delta-PLP4
 FT peptide
 FT 1..5
 FT /note= "synthetic N-terminal peptide not found in
 the native protein"
 FT region
 FT 9..20
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 11..31
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 42..62
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 43..60
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 45..58
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 49..70
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
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 FT 57..70
 FT /label= Eptope
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 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 69..82
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 71..104
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"

FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 93..105
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
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 FT 93..108
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
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 FT /label= Eptope
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 FT /label= Eptope
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 FT 127..138
 FT /label= Eptope
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 FT 127..140
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT 152..166
 FT /label= Eptope
 FT /note= "PLP epitope associated with MS"
 FT region
 FT 14..35
 FT /label= Eptope
 FT /note= "encephalitogenic epitope in mouse model"
 FT 57..70
 FT /label= Eptope
 FT /note= "encephalitogenic epitope in mouse model"
 FT region
 FT 93..105
 FT /label= Eptope
 FT /note= "encephalitogenic epitope in mouse model"
 FT peptide
 FT 170..173
 FT /label= Spacer
 FT 174..368
 FT /label= MBP21.5
 FT peptide
 FT 369..375
 FT /label= Histidine tag
 FT /note= "hexa-histidine tag facilitates recombinant
 protein purification"

W0634623-A1.
 PD 07-NOV-1996.
 PE 22-APR-1996; U05611.
 PR 02-MAY-1995; US-431648.
 PR 02-MAY-1995; US-431644.
 PR 07-JUN-1995; US-482114.
 PA (ALEX-) ALEXION PHARM INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Leonardo MJ, Matlis L, McFarland HF, Mueller EE, Mueller JP;
 PI Nye SH, Pelfrey CM, Squinto SP, Wilkins JA;
 DR WPI: 96-505898/50.
 DR N-PSDB: T41894.
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PT Claim 35; Page 113-114; 156pp; English.
 PS PM4 chimera (W06104) is a fusion protein composed of delta PLP4
 CC (W06101) and MBP21.5 (W00399). Delta PLP4 is a proteolipid protein
 CC (PLP) myelin that lacks all 4 hydrophobic domains of native human
 CC PLP (W06106) but includes PLP epitopes associated with multiple
 CC sclerosis (MS). MBP21.5 is a foetal isoform of human myelin basic
 CC protein (MBP) associated with MS. PM4 is in reverse orientation to
 CC MP4 chimera (W06103). It can be expressed in bacterial host cells
 CC using a DNA construct (T41894). PLP polypeptides (see also W00400,
 CC W06101-03 and W06105) can be used in the clinical assessment,
 CC diagnosis and treatment of MS.
 SQ Sequence 375 AA;

Query Match 97.0%; Score 894; DB 1; Length 375;
 Best Local Similarity 86.7%; Pred. No. 7.4e-87;
 Matches 170; Conservative 0; Mismatches 0; Indels 26; Gaps 1;

```

QY 2 ASQKRPSSQKRGKYLATASTMDHARHGFLPRHNDTGILDSIGRFFGGDRGAPKRGSG---58
DB 174 ASQKRPSSQKRGKYLATASTMDHARHGFLPRHNDTGILDSIGRFFGGDRGAPKRGSGKYP 233
QY 59 -----KDSHHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNITV 95
DB 234 WLKPGSRPLPSHARSQPGLCNMKDSHHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNITV 293
QY 96 TPRTPPPSQKRGKGLSLSRFSWGAEGORPGFGYGRASDYKSAHKFGKGVDAQGLTSKIF 155
DB 294 TPRTPPPSQKRGKGLSLSRFSWGAEGORPGFGYGRASDYKSAHKFGKGVDAQGLTSKIF 353
QY 156 KLGGRDSRSGSPMAR 171
DB 354 KLGGRDSRSGSPMAR 369

RESULT 13
ID R30736 standard; Protein: 170 AA.
AC R30736;
DT 21-MAY-1993 (first entry)
DE Human MBP.
KM Acetylcholine receptor; MHC; myelin basic protein; MBP.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 1
FT modified_site /note="N-Ac-Ala"
FT modified_site 107
FT modified_site /note="Me-Arg"
FT peptide 1..14
FT /note="claim 30; page 68"
PN WO9218150-A.
PD 29-OCT-1992.
PF 23-APR-1992; U03391.
PR 23-APR-1991; US-690840.
PA (ANER-) ANERGEN INC.
PI Clark BR, Lerch BL, Sharma SD;
DR MPI; 93-036056/04.
PT Pure major MHC-peptide complex - useful in treating deleterious
PT immune response such as autoimmunity
PS claim 30; Page 68 + fig 7; 93pp; English.
CC A method is claimed for the prepn. of a pure major MHC-peptide
CC complex. The MHC component is a class II glycoprotein of the MHC
CC and the peptide comprises amino acids 1-14 of MBP.
SQ Sequence 170 AA;

Query Match 96.6%; Score 891; DB 1; Length 170;
Best Local Similarity 98.2%; Pred. No. 5.9e-87;
Matches 167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ASQKRPSSQKRGKYLATASTMDHARHGFLPRHNDTGILDSIGRFFGGDRGAPKRGSGKDS 61
DB 1 ASQKRPSSQKRGKYLATASTMDHARHGFLPRHNDTGILDSIGRFFGGDRGAPKRGSGKDS 60
QY 62 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNITVTPRTPPPSQKRGKGLSLSRFSWGAEG 121
DB 61 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNITVTPRTPPPSQKRGKGLSLSRFSWGAEG 120
QY 122 QRRGFGYGRASDYKSAHKFGKGVDAQGLTSKIFKLGGRDSRSGSPMAR 171
DB 121 QRRGFGYGRASDYKSAHKFGKGVDAQGLTSKIFKLGGRDSRSGSPMAR 170

RESULT 14
ID R04717 standard; protein: 168 AA.
AC R04717;
DT 23-AUG-1990 (first entry)
DE Empirically determined sequence of myelin basic protein (MBP)
DE Myelin basic protein; multiple sclerosis; autoantigen; autoimmune disease;
DE epitope; myelin sheath.

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FH Key Location/Qualifiers
FT misc_difference 1
FT /label=OTHER
FT /note="N-Ac-Ala"
FT misc_difference 168
FT /label=OTHER
FT /note="Arg-COOH"
PN WO8912459-A.
PD 28-DEC-1989.
PF 23-JUN-1989; U02784.
PR 21-JUN-1989; US-367751, US-210594.
PA (BIOS-) Biospan Corp.
PI Sharma SD, Lerch LB, Clark BR;
DR MPI; 90-022384/03.
PT New complexes of histo-compatible glyco:protein -
PT with antigenic peptide(s) and label or toxin, used to target
PT antigen specific T helper cells
PS Fig 7; 74pp; English.
CC The patent claims complexes of formulae (I), (II) and (III) which are as
CC follows: (I) X - MCH - peptide; (II) MHC - peptide - X; (III) MHC -
CC peptide. Where X = toxin or labelling gp.; MHC = effective portion of the
CC major histocompatibility glycoprotein; and the peptide includes an
CC epitope associated with one of the major autoimmune diseases, including
CC multiple sclerosis (MS). MBP is the principle autoantigen in MS and is a
CC candidate peptide for insertion in the complexes which can be used to
CC treat and monitor MS. Pertinent sections of MBP are determined
CC empirically, using a strain of mice which develops experimental
CC allergic encephalitis when immunised with bovine MBP. The sequence
CC given in p94717 is with the substitution of the residues above the
CC sequence in fig 7. The sequence without substitutions is given in p92226.
SQ Sequence 168 AA;

Query Match 92.7%; Score 855; DB 1; Length 168;
Best Local Similarity 96.5%; Pred. No. 3.7e-83;
Matches 164; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 2 ASQKRPSSQKRGKYLATASTMDHARHGFLPRHNDTGILDSIGRFFGGDRGAPKRGSGKDS 61
DB 1 ASQKRPSSQ-HG-KYLATASTMDHARHGFLPRHNDTGILDSIGRFFGGDRGAPKRGSGKDS 58
QY 62 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNITVTPRTPPPSQKRGKGLSLSRFSWGAEG 121
DB 59 HHPARTAHYGSLLPQKSHGRTQDENPVVHFFKNITVTPRTPPPSQKRGKGLSLSRFSWGAEG 118
QY 122 QRRGFGYGRASDYKSAHKFGKGVDAQGLTSKIFKLGGRDSRSGSPMAR 171
DB 119 QRRGFGYGRASDYKSAHKFGKGVDAQGLTSKIFKLGGRDSRSGSPMAR 168

RESULT 15
ID R48594 standard; protein: 168 AA.
AC R48594;
DT 31-JUL-1994 (first entry)
DE Rabbit myelin basic protein.
DE Proteolipid protein; myelin basic protein; retrovirus;
DE neurological disease; by-stander antigen; TGF-beta;
DE transforming growth factor-beta; T-cell; T-lymphocyte;
DE myelopathy; paraparesis; human immunodeficiency virus type 1.
OS Oryctolagus cuniculus.
PN WO9404121-A.
PD 03-MAR-1994.
PF 17-AUG-1993; U07786.
PR 17-AUG-1992; US-931217.
PA (AUTO-) AUTOIMMUNE INC.
PI Hafner DA, Weiner HL;
DR MPI; 94-082786/10.
PT Treating retroviral associated neurological disease - by admin.
PT of by-stander antigen, causing release of transforming growth
PT factor beta from suppressor T cells
PS disclosure: Page 49; 64pp; English.
SQ Myelin basic proteins (sequences R48592-96) and cattle proteolipid

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CC protein (R48592) elicit the release of TGF-beta from suppressor T-
CC cells and target the T-cells to neural tissue under cytotoxic
CC attack, thereby reducing neurological disease, e.g. HTLV-1
CC associated myelopathy, tropical spastic paraparesis and HIV
CC infection.
SQ Sequence 168 AA;

Query Match 90.2%; Score 832; DB 1; Length 168;
Best Local Similarity 91.2%; Pred. No. 1e-80;
Matches 155; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 2 ASOKRPSORHSGSKYIATASTMDHARHGFLPRHRDPTGILDSIGRFFGSDRGAPKRGSGKDS 61
Db 1 ASOKRPSORHSGSKYIATASTMDHARHGFLPRHRDPTGILDSIGRFFSSDRGAPKRGSGKD- 59
QY 62 HHPARTAHYGSILPOKSHGRTODENPVVHFFKNIVTPRTPPSOGKRGSLSRFSGAEG 121
Db 60 -HAARTHYGSILPOKSHGRTODENPVVHFFKNIVTPRTPPSOGKRGSTVLSRFSGAEG 118
QY 122 QPQGFYGGRAADYKSAHKGKGVDAOGTLSKIEKLGGRDSRSGSPMAR 171
Db 119 QPQGFYGGRAADYKSAHKGKGVDAOGTLSKIEKLGGRDSRSGSPMAR 168

Search completed: September 26, 2000, 19:25:03
Job time: 5855 sec

